STIC-Biotech/ChemLib

From: Sent:

Rao, Manjunath N.

Thursday, June 26, 2003 11:20 AM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 09/762,767

Fr m: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date: 6-26-03

Please search the following as soon as possible for application with serial number 09/762,767

- SEQ ID NO:1 and 3, against all commercial nucleic acid databases including issued patents database and 1. pending application database and provide a print of all results.
- 2. SEQ ID NO: 2 and 4, against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. **Biotechnology Patent Examiner** Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO.

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Perfect score:
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ALIGNMENTS

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AAY70475;

AAY70475 standard; Protein; 690 AA

Human cyclic nucleotide-associated protein-3 (CNAP-3).

04-JUL-2000 (first entry)

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Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferative disorders (e.g. arteriosclerosis, cirrhosis, leukaemia, lymphoma and cancer of the breast, prostate, lung and brain), autoimmune/inflammattory disorders (e.g. actoma, anaemia, diabetes mellitus, multiple sclerosis and psoriasis), neurological disorders (e.g. epilepsy, Alzheimer's/Parkinson's disease and strokes), vision disorders (e.g. conjunctivitis, glaucoma, cataracts and retinitis pigmentosa), reproductive disorders (e.g. infertility, uterine fibroids, ectopic pregnancies and impotence) and smooth muscle disorders (e.g. angina, anaphylactic shock, Kearns-Sayre syndrome and hypertension). The coding sequence can be used for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous, reproductive, cardiovascular and developmental tissues. CNAP sequences may be used for prevention, treatment and diagnosis diseases associated with altered CNAP expression such as, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated protein-3 (CNAP-3), identified in Incyte clone 159278, that is isolated from ADENINBO1 cDNA library. It is expressed in
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                                                                      VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
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                                                      VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
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protein-3 (CNAP-3)
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Antibodies to hagCalphal/betal can be used for diagnosis of aberrant hagCalphal/betal expression in human tissues. This sequence represents the human soluble guanylylcyclase alphal subunit described in the method of the invention.
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                                                           KRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMPPCF
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Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated g
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08-DEC-2000;

08-DEC-2000;

24-JAN-2001;

16-MAR-2001;

16-MAR-2001;

16-APR-2001;

24-APR-2001;

30-APR-2001;
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                                                     BIOTECHNOLOGY INC
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                                DH,
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ABG61800-ABG61944 represent prostate cancer-associated proteins.
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QQGTNSKPCFQKKDVEDGNANFLGKASGID
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                                                                        VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
                                                                                                                                                 ESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNN
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RESULT 4
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                                                                         The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer are particularly useful in gene therapy, as a vaccine or in antisense applications.

C ABG61800-ABG61944 represent prostate cancer-associated proteins.
Query Match
Best Local S
Matches 625
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08-DEC-2000;
08-DEC-2000;
24-JAN-2001;
                                                                                                                                                                                                                                                                                                            Claim 27; Page 363; 436pp;
                                                                                                                                                                                                                                                                                                                                       Detecting a prostate cancer-associated transcript in a cell in patient, useful for diagnosing prostate cancer (PC) or screening modulators of Pc, by determining if prostate cancer-associated are expressed in a prostate tissue
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                                                      Sequence
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30-APR-2001;
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16-MAR-2001;
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DB; ABK92193.
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2000US-0733728.

; 2000US-0733748.

; 2001US-263957P.

2001US-276889.

; 2001US-276889.

; 2001US-281922P.

; 2001US-281922P.

; 2001US-288589P.
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               88.3%;
90.7%;
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Score 3171.5; DB 2
Pred. No. 1.1e-294;
0; Mismatches 37;
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11-JUL-2000;
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                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                   27-SEP-2001.
                                                                                                                           WO200171042-A2
                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                          pharmaceutical.
                                                                                                                                                                                         Drosophila;
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                                                                                                                                                                                                               melanogaster polypeptide
                                                                                                                                                                                      developmental
                                    2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                      biology; cell signalling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                 QEFLGSLDGVYDVLK----LQEED-----VTDTGFVCAGEGE----LIFTSERPVIAWLLL 189
                                  PRKINVSPTTYRLLKDCPGFVF -- TPRSREELPPNFPSEIPG -- - ICHFLDAYQ
                                                                       ALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV 612
                                                                                                                                                           EE-----YFEILTPK-INQTFSGIMTMLNMQFVVRVRRWDNSVKKSSRVMDLKGQMIY 372
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           ALKINVSPTTKDWLTKHEGFEFELQPRDPSFLPKEFPN--PGGTETCYFLESFR
                                                           ALKMIDACSKHITHDGEQIKMRIGLHTGTVLAGVVGRKMPRYCLFGHSVTIANKFESGSE
                                                                                                          ICSRATPFMVISMLEGLYKDFDEFCDFFDVYKVETIGDAYCVASGLHRASIYDAHKVAWM
                                                                                                                          ICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIALM
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117; Mismatches 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel purified human soluble guanylate cyclase alphal/betal (hsCcalphal/betal). The products of the invention have antiarteriosclerotic, vasotropic and hypotensive activity. Nucleic acid sequences encoding the alphal and/or betal subunit are useful for somatic gene therapy of arteriosclerosis and restenosis, ischemia (infarct), peripheral arterial occlusive disease and arterial hypertension. Antibodies to hsGcalphal/betal can be used for diagnosis of aberrant hsGCalphal/betal expression in human tissues. This sequence represents the human soluble guanylylcyclase betal subunit described in the method of the human soluble guanylylcyclase betal subunit described in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human soluble guanylate cyclase alphal/betal and the nucleic acid encoding the subunits, useful for producing diagnostic antibodies, and
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                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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specification,

The sequence data for this patent did not form

but was obtained in electronic format directly from ...pub/mublished not account.

WIPO

ftp.wipo.int/pub/published_pct_sequences

The invention relates to an isolated nucleic acid detection reagent

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Disclosure; SEQ ID

NO 1239;

21pp + Sequence Listing; English

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New isolated nucleic
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    27-SEP-2001
                                         WO200171042-A2
                                                                            Drosophila melanogaster.
                                                                                                                       pharmaceutical.
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Pred. No. 1.1e-61;
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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interactions
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                                                       YCLFGNNVTLANKFESCSVPRKINVSPTT-----YRLL------KDCPGFVFTPR
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                                                                                                                                                                         RAQDGLKKRLG---KLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQ--VVQA 474
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                    YCLFGDTVNTASRMESTSIAMKVHISESTKVLIGPNYKIIERGEIDVKGKGTMGTYWLEE
                                                                                              VAGAPDKDANHAERVCDMALDMVDAITDLKDPSTGQHLRIRVGVHSGAVVAGIVGLKMPR
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                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 5844; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                Sequence
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Best Local Similarity
Matches 114; Conserv
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N-PSDB; AAF89878.
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The present sequence represents soybean cyst nematode guanylyl cyclase-2 Themoreceptor, designated HG-gcy-2. HG-gcy-1 polynucleotides and polypeptides are useful as active agents for controlling plant feeding nematodes. They can be used to screen for compounds that have the ability to disrupt parasitic nematode feeding or chemotaxis.
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TLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREEL | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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chemotaxis; HG-gcy-2.
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Pred. No. 2.2e-34;
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RESULT 11
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guanylyl cyclase; GC-C; heat stable; mucosa; polyA+ RNA; PCR; enterotoxin binding domain; antibody; diarrhoea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAR38862-63 represent the guanylyl cyclases, GC-A and GC-B, which binds heat stable enterotoxin. These proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-272183/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR38863 standard;
                                                                                                                                                                                                                                                                                                                                         diarrhoea. The proteins may be used to isolate l for antagonists of toxin binding. This sequence represented in the specification.
                  613
                                                                                               858
                                                                                                                                                      798
                                                                                                                                                                                440
                                                                                                                                                                                                          738
                                                                                                                                                                                                                                    411 DVVLIGEQARAQD------GLKKRLGK---
                                                                                                                                                                                                                                                             113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating abnormal
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DL,
     PRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                                                               LQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL-HKESDTHAVQIALMALKMME 558
                                                                                                                                                  TQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTP
                                                                                                                                                                          HQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSP
                                                                                                                                                                                                      ELVLLMERCWAODPTERPDFGQIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLYEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterotoxin, partic. diarrhoea
                                                                     LSDEVMS----
                                                                                              MQVVTLLNDLYTCFDAIIDNFDVYKVETIGDAYMVVSGLPGRNGQRHAPEIARMALALL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTAARLESSSKPMRIHISTTINHFLVNVLG-GFVTQARGEI 1078
                                           --DAVSSFRIRHRPH-DQLRLRIGVHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGQ
                                                                                                                                                                                                                                                                                                                 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 3; 26pp;
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schulz S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0623033
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                                                                                                                                                                                                                                                                                                                 Ã,
                                                                                                                                                                                                                                                                          12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                         - PHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                       Score 460; Ub --,
Pred. No. 2.4e-34;
                                                                                                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterotoxin; rat; small intestine;
receptor; bacterial enterotoxin;
llgand; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                             The binding domain of the
                                                                                                                                                                                                                                                                                                                                                      , can be used to eliminate isolate ligands and to screen sequence is given as it is
                  642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in - used to develop
caused by bacterially
                                                                                                                                                                                                                                 -----LKATLEQA
                                                                                                                                                                                                                                                                                    Length 1025;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                         Gaps
                                                                                              916
                                                                                                                                                                             499
                                                                                                                                                                                                       797
                                                                                                                                                   857
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AAR10399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
    The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr.
                                                                                                                                                 WPI; 1991-036711/05.
N-PSDB; AAQ10324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                 Claim 3;
                                                                                                                                                                                                                                                                       22-JUN-1990;
                                                                                                                                                                                                                                                                                                                              WO9100292-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperaldosteronism;
                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                            23-JUN-1989;
                                                                                                                                                                                                                                                                                                   10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPRB;
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                                                                              F1g 1;
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Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 1047 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                          89US-0370673
                                                                                                                                                                                                                          90WO-US03586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNP; kidney failure;
ism; glaucoma; guanyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= cytoplasmic domain
/note= "GC and protien kind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        'label=
                                                                                                                                                                                                                                                                                                                                                                                                                      'label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label=
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                                                                                                                                                                                                                                                                                                                                                       label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l= N-glycos_site
English
                                                                                                                               Lowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "binds natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mature NPBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal sequence
                                                                                                                                                                                                                                                                                                                         N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                      N-glycos_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114,952). The protein (or variants) can be used in treatment constriuretic peptide disorders, and also to isolate peptides usin affinity chromatography. Antibodies with affinity for NPRB can also be prepd. An analogue, NPRBDKC, comprising only AAs 1-433 the mature protein, is also claimed, as well as variant describe in AAR10867.
                                                                                                                                                                                                                                                                                                                                                                                              AAR10867 standard; Protein; 1047
 Modified-site
                     Modified-site
                                           Modified-site
                                                                                     Modified-site
                                                                                                                                             Domain
                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                NPRB; ANP; BNP; CNP; hyperaldosteronism;
                                                                                                                                                                                                                                                                                                                                 NPRB(Pro655,
                                                                                                                                                                                                                                                                                                                                                       09-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                Modified-site
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                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSDEVMS-----PHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL-HKESDTHAVQIALMALKMME
:||:|:|| || || || ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQAYLEEKRKABALLYQILPHSVABQLKRGETVQABAPDSVTIYFSDIVGFTALSABSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVLIGEQARAQD------GLKKRLGK------LKATLEQA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALKIHVSSTTKDALDELGCFQLELRGDVEM 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQVVTLLNDLYTCFDAIIDNFDVYKVETIGDAYMVVSGLPGRNGQRHAPEIARMALALL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELVLLMERCWAQDPAERPDFGQIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLVEER
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ilarity 41.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                 Glu656,
                                                                                                                                                                                                                                                                                                                                                     (first entry)
244..246
/label- N
277..279
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479..1047
                                                                                                                                                                                                                                                                                              CNP; kidney failure; heart failure; ism; glaucoma; guanyl cyclase.
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                                                                                                                                                                /note= "binds
456..456
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12
                                            195..197
                                                                  161 . . :
                                                                                                                   /note- "GC and
                                                                                                                               /label-
                                                                                                                                                                                                /label= mature
23..455
                                                                                                                                                                                                                                                      Location/Qualifiers
                               /label=
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                                                                                               'label- N-glycos_site
                                                                                                                                                                                                                                                                                                                                Leu663,
          N-glycos_site
                               N-glycos_site
                                                     N-glycos_site
                                                                          N-glycos_site
                                                                                                                               cytoplasmic domain
                                                                                                                                                     transmembrane domain
                                                                                                                                                                                       extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                               Phe664, Ala682).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 460;
Pred. No. 2.
                                                                                                                                                                          natriuretic
                                                                                                                     protien
                                                                                                                                                                                                           NPBR
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.5e-34;
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                                                                                                                    activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1047;
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t described
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                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 113; Conserv
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                    The mutant was produced by modifying the DNA encoding the native sequence. The protein has guanyl cyclase (GC) activity protein kinase activity. The DNA can be inserted into express vectors for the prodn. of the NPRB analogue. The protein can used in treatment of natriuretic peptide disorders, and also t isolate peptides using affinity chromatography. Antibodies wi sefinity for NPRB can also be prepd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Editor's note: the AAs replaced in the sequence do not correspond to those of NPRB given in the specification (see p.27, 1.23-27; figs. 1 and 2), but instead to AAs in the sequence provided for NPRA (fig. 2). The origin of the AAs to be substituted is not clear; they may be taken from the sequence of rat NPRB (p.8, 1.18; p.9, 1.33) or rat NPRA (p.27, 1.20). The substitution indicated on p.9, 1.33, i.e. "Phe644" is thought to be an error and should read
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natriuretic protein receptor B - for diagnosis and kidney failure, heart failure, hyperaldosteronism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-036711/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of a variant of natriuretic peptide receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPRB
966
                          613
                                                        939
                                                                                  559
                                                                                                              880
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                                                                                                                                                                      820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Disclsoure; 49pp;
                                                                                                                                LQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL-HKESDTHAVQIALMALKMME
ALKIHVSSTTKDALDELGCFQLELRGDVEM
                          PRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                                 LSDEVMS-----PHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
                                                                                                             HOVYTLLNDLYTCFDAIIDNFDYYKVETIGDAYMYVSGLPGRNGQRHAPEIARMALALL-
                                                                                                                                                                     TQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTP
                                                                                                                                                                                  HQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSP
                                                                                                                                                                                                                           ELVLLMERCWAQDPAERPDFGQIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLVEER
                                                                                                                                                                                                                                                       DVVLIGEQARAQD----
                                                     --DAVSSFRIRHRPH-DQLRLRIGVHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGQ
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/label- N
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349..351
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41.9%;
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                                                                                                                                                                                                                                                                                Score 460; DB 12;
Pred. No. 2.5e-34;
9; Mismatches 76

    for diagnosis and treatment of
hyperaldosteronism, glaucoma etc

                                                                                                                                                                                                                                                         -GLKKRLGK-----
                          642
                                                                                                                                                                                                                                                                                   76;
                                                                                                                                                                                                                                                                                                            Length 1047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
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RESULT 14 AAR38862

995

genotyping;

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RESULT 15
AAU11280
ID AAU11
XX
AC AAU11
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DT 12-MP
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Best Local 9
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mucosa; p
binding d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAR38862-63 represent the guanylyl cyclases, GC-A and GC-B, which binds heat stable enterotoxin. These proteins are enterotoxin receptors which may be used as a therapeutic to control intestinal fluid permeation as well as abnormal conditions caused by bacterially released enterotoxin. The binding domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GC-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified enterotoxin receptor protein - used to develop prods. for treating abnormal conditions caused by bacterially released enterotoxin, partic. diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1993.
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      12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR38862;
                                 AAU11280;
                                                           AAU11280 standard; Protein; 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                      by bacterially released enterotoxin. The binding domain of the proteins, or antibodies to the proteins, can be used to eliminate diarrhoea. The proteins may be used to isolate ligands and to scr for antagonists of toxin binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR38862 standard;
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                                                                                                                                     962
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                                                                                                                                                                                                                                                                                                              782
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                                                                                                                                                                                                                                                                                                                                                                      102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l cyclase; GC-C; h
polyA+ RNA; PCR;
domain; antibody;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n,
                                                                                                                                                                                                                                                                                                        DNLLSRMEQYANNLEELVEERTQAYLEERRKAEALLYQILPHSVAEQLKRGETVQAEAFD
                                                                                                                                                                                                                                                  DGLKKRL----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFS
                                                                                                                                                               LEGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGEVETPRSREEL
                                                                                                                                                                                          PVRNGQLHAREVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVVGLKMPRYC
                                                                                                                                                                                                                       H-KESDTHAVQIALMALKMMEL--SDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYC
                                                                                                                                    LFGDTVNTASRMESNGEALK IHLSSETKAVLEEFDGFELELRGDVEM
                                                                                                                                                                                                                                                                                                                                                                                                                                1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schulz S;
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   (first
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    entry)
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                                                                                                                                                                                                                                                                                                                                                                                    12.7%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 457.5; DB 14, Pred. No. 4.2e-34; 0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
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receptor; bacterial
ligand; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                Length 1029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         small intestine;
                                                                                                                                                               642
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                                                                                                                                                                                                                                                                               538
                                                                                                                                                                                                                                                                                                           841
                                                                                                                                                                                                                                                                                                               CC ancoding the human natriuretic peptide receptor A/guanylate cyclase A CC (atrionatriuretic peptide receptor A) or NPR1 polypeptide. A method for CC haplotyping the NPR1 gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one CC of the copies of the gene is defined by one of the NPR1 haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype cc pairs can be assigned to specific genotypes. An association between a CC identified by comparing the frequency of the NPR1 gene can be critical and a haplotype or haplotype pair of the NPR1 gene can be comparing the trait with the frequency of the haplotype pair in a reference population, where a higher haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype pair. NPR1 and its corresponding DNA are used for studying the expression and function of NPR1, for use in screening cc chypertension. The sequences are also useful for studying the effect of variation on the biological activity of NPR1 as well as on the binding affinity of candidate drugs targeting NPR1. This sequence represents the
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Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of an individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of the gene •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atrionatriuretic peptide receptor A; haplotyping; cytostatic; haplotype pair; single nucleotide polymorphism; gene therapy; drug screening; hypertension; hypotensive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bentivegna SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2001;
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                                                                                                                                  479
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DB; AAS16995.
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                                                                                                                                                                                                                                                                                                         ity of candidate drugs targeting NPR1. This sequence represents
NPR1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; F1g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                natriuretic
                                                                                                                                                                                                                                   Similarity
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LFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                                                  DGLKKRL----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFS
                                          PVRNGRLHACEVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVVGLKMPRYC
                                                                     H-KESDTHAVQIALMALKMMEL--SDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYC
                                                                                                                               NVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL
                                                                                                                                                             DNLLSRMEQYANNLEELVEERTQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFD
                                                                                                                                                                                                                                                                               1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide receptor A/guanylate
                                                                                                                                                                                                                                  12.78;
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                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                   Score 456.5; DB 2
Pred. No. 5.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor A (NPR1) protein
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                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nandabalan
                                                                                                                                                                                                                       78;
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                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                 Length
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Gaps

538

873

Search completed: June 27, 2003, 13:03:00 Job time: 39:3713 secs

994 LFGDTVNTASRMESNGEALKIHLSSETKAVLEEFGGFELELRGDVEM 1040

뭥

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 13:03:07; Search time 19.5034 Seconds (without alignments) 3401.080 Million cell updates/sec

Title: Perfect score:

Sequence: US-09-762-767A-2 3593 1 MFCTKLKDLKITGECPFSLL.....QKKDVEDGNANFLGKASGID 690

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	₅	4	ω	2	1	No.	Result
438	440	442	448	449.5	452	454.5	456.5	457.5	457.5	460	460	460	463.5	493.5	551.5	581	582.5	LT.	749.5	774.5	789.5	793.5	795	976.5	1635	3107.5	3171.5	3232	Score	
12.2	12.2	12.3		•	12.6	•	•	12.7	•	12.8	•	•	•	•	•			16.3				•	22.1	27.	45.	86.5	88.	90.	Match 1	Query
1108	1103	BOLT	1108	1057	1100	1057	1061	1057	1057	1047	1047	1047	1057	583	699	1099	686	685	751	682	619	619	619	683	732	691	717	690	Length I	
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в55915	JC5581	I59385	A55915	OYMSAR	T42260	157963	OYHUAR	I55319	OYRTR	145882	OYRTBR	OYHUBR	T15720	F88642	T18984	T16822	T23721	T19968	T24458	OYRTB2	S23097	OYB070	OYRTB1	JH0810	S18325	OYB077	S23098	OYRTAL	ID	
				atrial natriuretic	guanylate cyclase	natriuretic peptid	natriuretic peptid	guanylyl cyclase A	atrial natriuretic	guanylate cyclase	atrial natriuretic	natriuretic peptid	hypothetical prote						0							cyc	cyc	ylate cyclase	Description	

44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
412.5 411.5	414	418	418	420.5	423.5	427	428	428.5	428.5	430	434	435	436	438
11.5 11.5	11.5	11.6	11.6	11.7	11.8	11.9	11.9	11.9	11.9	12.0	12.1	12.1	12.1	12.2
1122 540	1144	1170	1012	1005	1525	1125	1068	1130	1050	1110	632	1102	632	1110
20	N	N	Ν	N	۳	_	N	Ŋ	N	2	N	N	N	-
T28130 T34187	T21223	T27564	T24384	S33525	A56699	OYURCP	T42382	A89130	S45636	I59370	T31667	JH0717	T31666	S55279
hypothetical prote hypothetical prote	_	hypothetical prote	hypothetical prote	guanylate cyclase	guanylate cyclase	speract receptor p	guanylate cyclase	protein F52E1.4 [i	natriuretic-peptid	guanylate cyclase	guanylate cyclase	guanylate cyclase	natriuretic peptid	guanylate cyclase

ALIGNMENTS

Query Match 90.0%; Score 3232; DB 1; Length 690; Best Local Similarity 89.1%; Pred. No. 4.6e-217; Matches 616; Conservative 39; Mismatches 34; Indels 2; Gaps 2;	RESULT 1 OVERTAL OVERTAL QUANTIATE cyclase (EC 4.6.1.2), soluble, alpha-1 chain - rat N.Alternate names: guanylate cyclase, soluble, 77K chain C.Species: Rattus norvegicus (Norway rat) C.Accession: A38297 C.Accession: A38297 R.Nakane, M.: Arai, K.; Saheki, S.; Kuno, T.; Buechler, W.; Murad, F. J. Biol. Chem. 265, 16841-16845, 1990 A.,Title: Molecular cloning and expression of cDNAs coding for soluble guanylate cyclase, Reference number: A38297; MUID:91009100; PMID:1698769 A.; Molecula type: mRNA A.; Residues: 1-690 <anx- -="" <ccc="" a.;="" biosynthesis;="" c.;="" c.keywords:="" catalytic="" cgmp="" cross="" cyclase="" cyclase;="" domain="" domain:="" f:432-660="" gb:m36075;="" gb:m57405;="" guanylate="" heterodimer;="" homology="" lyase="" nid:9204277;="" phosphorus-oxygen="" pid:9204278="" pidn:aaa41206.1;="" references:="" soluble="" superfamily:=""></anx->
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Qy	Db	Qy	₽	Qy	Db	Qy	Db	Qy	Db	Qy	Дb	Qy	DЬ	Qy	Marches
421 AQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNV 480	360 SRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQAR	- 20	300 LGNGIRRLYNKRDFQGKPNFEEFFEILTPKINQTFSGIMTMLNMQFVIRVRRWDNLYKKS	04	240 RSECTEFVNQPYLLYSVHVKSTKPSLSPGKPQSSLVIPTSLFCKTFPFHFMLDRDLAILQ	241 HNDCSEFVNQPYLLYSVHMKSTKPSLSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTILQ 300	180 RRGRLEDASILCLDKDQDFLNVYYFFPKRTTALLLPGIIKAAARILYESHVEVSLMPPCF 2		120 EAIAAGVPVEVLKDSIGEELFKICYEEDEHIIGVVGGTLKDFLNSFSTLLKQSSHCQEAE 1	O	60 QRKTSRNRVYLHTLAESIGKLIFPEFERLNLALQRTLAKHKIKENRNSSEKEDLERIIAE 1	L-3	1 MFCRKFKDLKITGECPFSLLAPGQVPTEPIEEVAGVSESCQATLPTCQEFAE-NAEGSHP 59	EKNIQESLP	s oro; conservative 35; mismatches 34; indexs 2; baps
80	419	420	359	360	299	00	239	240	179	180	119	120	9	60	2

```
RESULT 2
$33098

guanylate cyclase (EC 4.6.1.2), soluble, 81K chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: $23098
R;Gluil1, G; Scholl, U; Bulle, F; Guellaen, G.
FEBS Lett. 304, 83-88, 1992
A;Title: Molecular cloning of the cDNAs coding for the two subunits of solubl
A;Reference number: $23097; MUID:92316204; PMID:1352257
A;Accession: $23098
A;Molecule type: mRNA
A;Residues: 1-717 <GIU>
A;Cross-references: EMBL:X66534; NID:g31683; PIDN:CAA47145.1; PID:g31684
C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain
C;Keywords: heterodimer; phosphorus-oxygen lyase
F;430-658/Domain: guanylate cyclase catalytic domain homology <GCC>
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OYBO77
guanylate cyclase (EC 4.6.1.2), solubre, guanylate cyclase, solu N;Alternate names: guanylate cyclase, solu C;Species: Bos primigenius taurus (cattle) C;Date: 30-Sep-1991 #sequence_revision 30 C.accession: $10713; A38767
Accession: Harteneck, C.; Humbert, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: Sivily, C;
R; Koesling, D.; Harteneck, C;
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R; Ko
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F; 434-662/Domain:
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A; Residues: 118-133;226-232;286-293;319-330;412-417;557-571;629-637 <R
A; Residues: 118-133;226-232;286-293;319-330;412-417;557-571;629-637 <R
C; Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic
C; Keywords: cGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
F;434-662/Domain: guanylate cyclase catalytic domain homology <GCC>
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A;Title: The primary structure of the larger subunit of A;Reference number: S10713; MUID:90306336; PMID:1973124
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A; Molecule type: mRNA
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Pred. No. 2.1e-208;
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Db 314 ADLRISINTECRAFPEHLMEDPSMSVLQLGEGLRKQL-RCDTHKVLKFEDCFEIVSPKVN 372 Qy 33 QTFSGIMTMLNNQFVVRVRRWDNSVKKSSRVNDLKGQMIXIVESSALLFLGSBCVDRLED 392	EREDFEKTIAEQAVAAGVPVEVIKESLGEEVFKICYEEDENILGVVGGTIKDFIN	S; Conservative 100 GECPFSLLAPGOV GECPLSRLCWNGSRSPPG RSRVYLHTLAESICKLIFPH	SULT 4 8325 Raylate cyclase, soluble, alpha chain - huma species: Homo sapiens (man) Date: 13-Jan-1995 #sequence_revision 13-Jan-Accession: S18325 Harteneck, C.; Wedel, B.; Koesling, D.; Malk BS Lett. 292, 217-222, 1991 Title: Molecular cloning and expression of a Reference number: S18325; MUID:92070494; PMI Accession: S18325 Status: preliminary Molecule type: mRNA Residues: 1-732 <harp (cross-references:="" embl:x63282;="" f="" nid:g31670;="" nid:g316<="" th=""><th> </th></harp>	
Qy 323YEEILTPK-INQTESGIMTMLNMQFVVRVRRWDNSVKKSSRVMDLKGQMIYIV 374		Query Match 27.2%; Score 976.5; DB 2; Length 683; Best Local Similarity 37.3%; Pred. No. 5.1e-60; Matches 244; Conservative 116; Mismatches 211; Indels 83; Gaps 20; Oy 58 SLPQRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESR 106 1	RESULT 5 JH0810 guanylate cyclase (EC 4.6.1.2) - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 26-Aug-1999 C;Accession: JH0810 R;Coshikawa, S.; Miyamoto, I.; Aruga, J.; Furuichi, T.; Okano, H.; Mikoshiba, K. J. Neurochem. 60, 1570-1573, 1993 A;Title: Isolation of a Drosophila gene encoding a head-specific guanylyl cyclase. A;Reference number: JH0810; MUID:93203896; pMID:8095978 A;Accession: JH0810 A;Molecule type: mRNA A;Residues: 1-683 <yos> A;Cross-references: GB:S57126; NID:9298674; PID:9298675 A;Experimental source: head C;Genetics: A;Gene: dgc 1 A;Cross-references: FlyBase:FBgn0010227 C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology C;Keywords: CGMP biosynthesis; phosphorus-oxygen lyase F;417-641/Domain: guanylate cyclase catalytic domain homology</yos>	Qy 453 LLCSIEPCEVAQQLWQGQVVQAKKPSNVTMLFSDTVGETAICSQCSPLQVITMLNALYTR 512

В

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guanylate cyclase (EC 4.6.1.2), soluble, beta-1 chain - rat N; Alternate names; guanylate cyclase, soluble, 70K chain C; Species; Rattus norvegicus (Norway rat) C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_cha C; Accession: A31871 R; Nakane, M; Saheki, S; Kuno, T; Ishii, K; Murad, F. Biochem. Blophys. Res. Commun. 157, 1139-1147, 1988 A; Title: Molecular cloning of a cDNA coding for 70 kilodalta A; Reference number: A31871; MUID:89087429; PMID:2905128 A; Accession: A31871
A; Molecule type: mRNA a. Data A; Mol
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A; Cross-references: GB: M;
C; Superfamily: soluble gu;
C; Keywords: GMP blosyntt
F; 373-607/Domain: guanyla
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    --VYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHS
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34.3%;
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C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic C;Superfamily: soluble guanylate cyclase; phosphorus-oxygen lyase C;Keywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase F;373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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A;Residues: 1-619 <ROE>
A;Cross-references: EMBL:Y00770; NID:g407; PIDN:CAA68739.1;
A;Cross-on: A:8759
A;Accession: A:8759
A;Molecule type: protein
A;Residues: 1-6;28-32;41-45;96-109;337-343;396-406;562-569
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THAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTL
                                                                                               TAICSQCS----PLQVITMLNALYTRFDQQCGELD---VYKVETIGDAYCVAGGLHKESD
                                                                                                                                                           VVGGTLKDFLNSFSTLLKQSSHCQEAGKRGRLEDASILCLDKE-DDFLHVYYFFPKRTTS
                                                                   NAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCI
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homology

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guanylate cyclase (EC 4.6.1.2), soluble, 70K chain C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S23097 R;Giuili, G.; Scholl, U.; Bulle, F.; Guellaen, G. FEBS Lett. 304, 83-88, 1992 R;Title: Molecular cloning of the cDNAs coding for A;Reference number: S23097; MUID:92316204; PMID:135 A;Accession: S23097
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C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic
C;Keywords: heterodimer; phosphorus-oxygen lyase
F;373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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Blochemistry 29, 10872-10878, 1990
A;Title: A new form of guanylyl cyclase is preferentially expressed in A;Reference number: A36228; MUID:91105012; PMID:1980215
A;Accession: A36228
A;Accession: A36228
A;Accession: A36228
A;Accession: GBC28
A;Accession: A36228
A;Cross: references: GB:M57507; GB:J05308; NID:g204279; PIDN:AAA41207.1
A;Experimental source: kidney
C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic C;Superfamily: soluble guanylate cyclase; phosphorus-oxygen lyase
F;360-584/Domain: guanylate cyclase catalytic domain homology <GCC>
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RESULT 10
724458
hypothetical protein T04D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
C;Accession: T24458
R;Kershaw, J.
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Pred. No. 5.9e-46;
                                                      15-Oct-1999 #text_change 04-Mar-2000
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C;Species: Caenorhabditis el
C;Date: 15-Oct-1999 #sequenc
C;Accession: T19968; T23092
R;Lennard, N.
submitted to the EMBL Data L
A;Reference number: Z19205
A;Accession: T19968
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A; Reference number: :
A; Accession: T24458
A; Status: preliminary
                                               T19968
hypothetical protein C46E1.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C; Date: T19968; T23092
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A; Residues: 1-751 <WILL>
A; Cross-references: EMBL: Z81114;
A; Cross-referental source: clone T04E
C; Genetics:
A; Gene: CESP: T04D3.4
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A; Introns: 1/3; 26/2; 9
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Best Local Similarity
Matches 192; Conserv
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31.5%; Pred. No. 3.7e-44;
tive 125; Mismatches 239
                                Library,
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Ylate cyclase;
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                                                                                #text_change
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domain
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RESULT T23721

hypothetical protein M04G12.3 - CC; Species: Caenorhabditis elegans

Caenorhabditis elegans

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R; Lennard, N.

R; Lennard, N.

submitted to the EMBL Data
submitted to umber: Z19673
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A; Introns: 11/3; 36/2;
C; Superfamily: soluble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z99942; PIDN:CAB17073.1; GSPDB:GN00028; A;Experimental source: clone H13N06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-685 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T23092
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   624
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                                                                                AGVVGVKMPRYCLEGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREE---
                                                                                                                                                                                        QLKQGLSVEAREYEEATVMFTDVPTFQQIVPLCTPKDIVHLLNELETKFDRLIGIQKAYK
                                                                                                                                                                                                                                                       F--QGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRWD-----NSVKKSSRVMD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSLEREDFEKTIAEQAV-------AAGVPVEVIKESLGE--EVFKICYEED--
 GKGEMNTYFLLRSFKRSIWEIIDRRRDENCNSIDGYNELREGYVDDVLNKVTQKNSKTC
                                                                                                                             VETVGDSYMSVGGIPDLVDDHCEVICHLALGMVMEARTVCDPITNTPLHIRAGIHSGPVV
                                                                                                                                                         VETIGDAYCVAGGLHKESDTHAVQIALMALKMMELSDEVMSP-HGEPIKMRIGLHSGSVF
                                                                                                                                                                                                                      QLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSNEEALGTAVVQHSNNYKIRLTHMDFISTFPYHMVVDQDCKIVQVG----RELYNHIPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSTKPSLSPSKPQSSLVIPTSL----FCKTFPFHFMFDKDMTILQFGNGIRRLMNR--RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRPGLYPIVKGVLREAAKRVFKLDVSMTITGRTQRSVQMATGERIEE-HVIFLVKTLNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKRTTSLILPGIIKAAAHVLYETEVEVSL---MPPCFHNDCSEFVNQPYLLYSVHM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVLERAGFEAG-KENIINHYYSDADTFSLVDAVSVILKVTREQVWEMYGCFLIQYTMETG
                                                              AGVVGAKMPRYCLFGDTVNTSSRMESHSPIGRIHCSENAKKCAESTGRFEFEPRGRVQIK
                                                                                                                                                                                                                                                                                     IHNALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDDLIRSMSPNLKGFLDNLDSLHYFIDHVVYKANLRG----PSFRCEDNPDGTITLHYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -ENILGYVGGTLKDFLNSFSTLLKQSSH-CQEAGKRGRLEDASILCLDKEDDFLHVYYFF
                                                                                                                                                                                                                                                                                                                    SENLYEDNNGALALSQSQHLKLKGQMMLMSSGGHIMYLCSPYVTSIPELLQYGLRLTAMP
                                                                                                                                                                                                                                                                                                                                                                                  LLSVGTP-LMRIFEVTRPQIPLDFDSICNFINAVFVLQVKTTPMEFQRNANKRAAQAIEA
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                                  ·LPPNFPSEIPGI--
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28.1%;
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Pred. No. 6.8e-33;
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domain homology
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T07D1

Length 1099; Indels

474/3; 523/3

CESP: TO

146;

Gaps

118

164 19

162 223

276

216

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C; Date: 15-Oc
C; Accession:
R; Sims, M.
     RESULT 13
T16822
RESULT 13
Protein T07D1.1 - Caenorhabditis
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-
C;Accession: T16822
R;Leimbac, D.
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A; Introns: 1/3;
C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T23721
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sion: T23721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIH----ESIRQLVIRKYGE-DVWLQ-VLERSGFENGKENIVNHYYSDTDTYVLVDSVSIV
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                                                                                                                                                                                                                                       ARSVMDPVNKTPFLLRIGLHSGTIIAGVVGTKMPRYCLFGETVTLASQMESLGVAGKIQC
                                                                                                                                                                                                                                                             SDEVMSP-HGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINV
                                                                                                                                                                                                                                                                                                            KNIVKLLNEVFFKLDRIVVLRGVYKVETVSDSYMTVSGIPDYTSEHAENMCHVALGMMWE
                                                                                                                                                                                                                                                                                                                               LQVITMLNALYTREDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMEL :: :|| :: :|| :| :|| ||
                                                                                                                                                                                                                                                                                                                                                                                    THELEVERQKTDSILKDMLPRKIAKQLLSGEHLEPCEY-EATVMFCDLPAFQQIIPVCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVLQVKTSPLRKKHMNAMTKEEREQEVEAMEEEVESNELTQGCHLKLKGQMMMLSTKKHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPYHFVLDESCRLVQCGDELYNHIPNELLQPGTPILRIFEINRPQIPLDFENICNFINAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHNDCSEFVNQP--YLLYSVHM-----KSTKPSLSPSKPQSSLVIPTSL-----FCKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRLEDASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLM---PPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKVTKDQIWEMYGGFLITYSMEIGWDELVRSMSPNLKGFLDNLDSLHYFIDHVVYKANLR
                                                                                                                                                                   SSWTYSKAMETGRFEFSPRGR
                                                                                                                                                                                                     SPTTYRLLKDCPGFVFTPRSR
                                                                                                                                                                                                                                                                                                                                                                                                                       HQALEBEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYLCSPYVTSINELMQFGMRLTAMPLHDATRDLILLNQQRLSDVEVNLQLEANNEQLETM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKRLGKLKATLEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 26/2; 60/1; 192/3; 255/2; 321/2; 401/2; 645/1 soluble guanylate cyclase; guanylate cyclase catalytic
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A, Description: The sequence of C. elegans cosmid T07Dl
A; Reference number: Z18584
A; Accession: T16822
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1099 <LEI>
A; Residues: 1-1099 <LEI>
A; Cross-references: EMBL:U41531; NID:gl109802; PID:gl1
C; Genetics:
A; Gene: CESP:T07Dl.1
A; Introns: 26/3; 94/3; 144/2; 200/3; 239/2; 278/3; 344
                                                                                      RESULT 14
T18984
hypothetical protein C06B3.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to
C;Accession: T18984
R;Percy, C
submitted to the EMBL Data Librar:
A; Reference number: Z19056
A; Accession: T18984
A; Status: preliminary; translated
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                            SPITYRLLKDCPGFVFTPRSREEL 642
                                                                                                                                                                                                                                                                                                                                                    LSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINV
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Pred. No. 3
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3.4e-32;
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04-Mar-2000

619 618 564 444 447 393 397 339 276 309

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A; Residues: 1-699 <WIL>
A; Cross-references: EMB|
A; Experimental source: C; Genetics:
                                                                                                                                                                                                            protein C54E4.3 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 C;Accession: F88642 R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
                                                                                                                  A; Note: published errata appeared A; Accession: F88642
                                                                                                                                A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology R;Reference number: A75000; MUID:9969613; PMID:9881916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ela.
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A:Introns: 1/3; 60/1; 192/3; 210/2; 270/2; 336/2; 415/2; 659/1
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic
                                                         A; Residues:
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                            ;Molecule type: DNA;Residues: 1-583 <570>;Residues: 1-583 <570>;Cross-references: GB:chr_IV; PIDN:AAB92031.1;
                                                                                             Status: preliminary
Genetics:
                    Note: Similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSR 639
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                  to guanylate
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                                  PID:g2702405;
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A;Gene: C54E4.3 A;Map position: 4

Š В Ş 밁 Ş 밁 Š 밁 δÃ 밁 Š 밁 S 밁 Ş 밁 δÃ 밁 Š Query Match Matches 139; Local 458 451 338 338 578 S 578 619 S 619 518 560 500 398 391 222 167 278 282 241 107 122 AVAAGVPVEVIKESLGE-EVFKICYEEDENILGVVGGTLKDFLNSFSTLLKQSSHCQEAG 181 KRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMPPCF 50 Similarity AKQVVVPKLERSVRLRIGVHCGPVVAGIVSQQKPRFCVLGNTVNVTKSICSHSSPGKVLV SDEVMSPHGE-PIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINV
: :|: | | : ::|||:| | | | | : | DRLLFEFVPPVIAEALRAAKTVPALMQKRISIDFSEEFSDCSVIFTDIPDFFTISVNCSP VDLLCSIFPCEVAQQLWQGQVVQA------KKFSNVTMLFSDIVGFTAICSQCSP EDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKT IMTMLNMQFVVRVRRWD--NSVKKSS-----RVMDLKGQMIYIVESSAILFLGSPCVDRL FCKTFPFHFMFDKDMTILQFGNGIRR---LMNRRDFQGKPNFEEYFEILTPK-INQTFSG ERRKSGMVE--HVIFSVEPDDNHRKGKRLFHKFRNTKTTENAPSFTLS---STILVGLRD TEIITVVTDLFHRFDRIIEKHKGYKVLSLMDSYLIVGGVPNANQYHCEDSLNLALGLLFE LQVITMLNALYTREDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMEL VLSYLNTLFIFQLKHHSKRNEVQEGSSEAFQQPLVLKGEMMPINDGNSIIFICSPHVTTV FKNIFPYHVCFNKQMIIEHIGIYLLREYGLENKKTLK----VSDLMQLVQPSDIQLTYKN HNDCSEFVNQPYLLYSVH------FKSEMKGPTFQCEPFGESGLKLHYFSFRQGLFPIVKGLVRKTARTLFEMDVKVCMLERNQ RDILNLKLYISDMPMHDATRDLYMLNQSRICQMELNKKLEETMKKMKKMTEELEVKKSQT ATVLGLSVDDMWEMYGEFLITHACETGWQKMLFCMANNLQEFLDNLNSM---HYFIDQIA Conservative 13.7%; 25.7%; 129; Score 493.5; DB 2 Pred. No. 1.8e-26; Mismatches ---MKSTK-----PSLSPSKPQSSLVIPTSL 218; 2 Length 583; Indels 55; 577 618 517 559 499 450 180 457 397 337 390 277 337 221 281 240 106 13;

Search completed: June 27, 2003, 13:05:23 Job time: 21.5034 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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4086.601 Million cell updates/sec

US-09-762-767A-2 3593

Title:
Perfect score:
Sequence: 1 MFCTKLKDLKITGECPFSLL.....QKKDVEDGNANFLGKASGID 690

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : sp_archea:*
sp_bacteria:*
sp_tung1:*
sp_human:*
sp_invertebrate:*
sp_manuma1:* sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle:*
sp_phage:* sp_plant:*
sp_rodent:*
sp_virus:* p_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	o	Us	4	w	2	r	Result
781	781.5	784.5	785.5	788	823	985.5	991.5	1097	2005	2009.5	2014.5	2954	3265.5	3266.5	3587	Score
21.7	21.8	21.8	21.9	21.9	22.9	27.4	27.6	30.5	55.8	55.9	56.1	82.2	90.9	90.9	99.8	Query Match Length DB
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P79998 oryzias lat	O54865 mus musculu	Q91xj7 rattus norv	077106 manduca sex	Q90vy5 fugu rubrip	Q8r514 rattus norv	Q95sq4 drosophila	Q24085 drosophila	077105 manduca sex	Q90vv5 fugu rubrip	P79997 oryzias lat	Q9pwi2 oryzias lat	Q9nnw8 homo sapien	Bum	Q9dbq3 mus musculu	Q8tah3 homo sapien	Description

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
452	453	453.5	454.5	455.5	456.5	460	460	461	462	463.5	473	477	478	479	493.5	547	551.5	555	582.5	587	642.5	661	720.5	743	743	749.5	750.5	771.5
12.6	12.6	12.6	12.6	12.7	12.7	12.8	12.8	12.8	12.9	12.9	13.2	13.3	13.3	13.3	13.7	15.2	15.3	15.4	16.2	16.3	17.9	18.4	20.1	20.7	20.7	20.9	20.9	21.5
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181 KRGRLEDASILCLDKEDDFLHVYYEFPKRITSLILPGIIKAAAHVLYETEVEVSLMPPCF 240 	121 QAVAAGVPVEVIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFSTLLKQSSHCQEAG 180	121 QAVAAGVPVEVIKESIGEEVFKICYEEDENIIGVVGGTLKDFLNSFSTLLKOSSHCQEAG 180	61 QRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESRKSLEREDFEKTIAE 120	61 QRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESRKSLEREDFEKTIAE 120	1 MFCTKLKDLKITGECPFSLLAPGQVPNESSEEAAGSSESCKATMPICQDIPEKNIQESLP 60	1 MFCTKLKDLKITGECPFSLLAPGQVPNESSEEAAGSSESCKATVPICQDIPEKNIQESLP 60	Query Match 99.8%; Score 3587; DB 4; Length 690; Best Local Similarity 99.7%; Pred. No. 1.6e-272; Matches 688; Conservative 2; Mismatches 0; Indels 0; Gaps	SEQUENCE 690 AA; 77470 MW; D9B98FC0E4DBB927 CRC64;	028384; AAH28384.1;	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.	Strausberg R.;		SEQUENCE FROM N.A.		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBT TaxTD=9606:	Chordata;	Homo sapiens (Human).	quanylate cyclase	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	(Tremburel 21,		Q8TAH3 PRELIMINARY; PRT; 690 AA.	H3	זת 1
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RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Fukunishii Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishii Y., Konno H., Kasukawa T., Saito R.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishii Y., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsud Y., Nishido I., Bono H., Kasukawa T., Saito R.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Hayashizaki Y.;
"Functional annotation of
Nature 409:685-690(2001).
EMBL; AK004815; BAB23586
HSSP; P19687; IAWN.
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Mammalia; Eutheria;
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                            BAB23586.1;
                                                                               of a
                                                                               full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                               mouse
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on update)
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GUCY1A3.

Mus musculus (Mouse) Eukaryota; Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

O9ERL9 PRELIMINARY; PRT;
O9ERL9;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last seq
O1-MAR-2002 (TrEMBLrel. 20, Last ann
SOluble guanylyl cyclase alpha 1 sub

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Best Local
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InterPro; IPR001054; G_cyclase.
Pfam; pF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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                                                                                                                                                                                                           TMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHR
                                                                                                                                                                                                                      TMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHK
                                                                                                                                                                                                                                                                                                                        FGNGIRRLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKKS
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                                                                                                            HHQGPNSKPWFQDKDVEDGNANFLGKASGID
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GUANYLATE_CYCLASES_2;
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Pred. No. 2.1e
36; Mismatches
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Best Local S
Matches 619
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InterPro: IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sharina I.G., Krumenacker J.S., Martin E., Murad F., "Genomic organization of alpha 1 and beta 1 subunits soluble guanylyl cyclase genes."; Proc. Natl. Acad. Sci. U.S.A. 97:10878-10883(2000). EMBL; AF297082; AAG17446.1; -. HSSP; P19687; 1AWN.
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NCBI_TaxID=10090;
[1]
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619; Conser
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                                                                                        ESDTHAVQIALMALKAMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNN
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HHQGPNSKPWFQDKDVEDGNANFLGKASGVD
          -QQGTNSKPCFQKKDVEDGNANFLGKASGID
                                                                              ESDTHAVQIALMALKMMELSNEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNN
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                                        VTLANKFESCSVPRKINVSPTTYRLLKDCPGEVFTPRSREELPPNFPSDIPGICHFLDAY
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Pred. No. 2.5e
97; Mismatches
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Best Local S
Matches 564
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Zhou Y.H.;

Zhou Y.H.;

Zhou Y.H.;

Submitted (FEB-2000) to the EMBL/G

EMBL; AF233750; AAF64043.1; JOINED

EMBL; AF233746; AAF64043.1; JOINED

EMBL; AF233747; AAF64043.1; JOINED

EMBL; AF233749; AAF64043.1; JOINED

EMBL; AF233749; AAF64043.1; JOINED

EMBL; AF233749; AAF64043.1; JOINED

HSSP; P19667; TANN.

InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.

SMARR; SM00044; CYCC; 1.
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NON_TER
SEQUENCE
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01-OCT-2000 (TrEMBLrel. 20, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
soluble guanylate cyclase large subunit (Fra
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NNW8;
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MEDLINE=20183694; PubMed=10717483;

Zhou Y.H., Zheng J.B., Gu X., Li W.H., Saunders G.F.;

Zhou Y.H., Zheng J.B., Gu X., Li W.H., Saunders G.F.;

"A novel Pax-6 binding site in rodent B1 repetitive elements:
coevolution between developmental regulation and repeated ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 245:319-328(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00452;
PS50125;
                                                                                                                                                                                                        DASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMPPCFHNDCSE
                   KRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKESNVTMLFSD
                                                                                                                           KGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLK
VQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANK
                                                                                                               KGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLK
                                                                                                                                                              RLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKKSSRVMDL
                                                                                                                                                                           RLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKKSSRVMDL
                                                                 KRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSD
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564 AA;
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GUANYLATE_CYCLASES_2;
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63406 MW;
                                                                                                                                                                                                                                                                                                                                                            82.2%; Score 2954; DB 4; 1
100.0%; Pred. No. 4.9e-223;
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RESULT
Q9PWI2
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Best Local S
Matches 403
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J. Biol. Chem. 274:18567-18573(1999).
EMBL; AB022280; BAA76690.1; -.
Interpre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001054; G_cyclase.
pfam; pF00211; guanylate_cyc; 1.
SMART; SM00044; CYC; 1.
PR0SITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble guanylyl cyclase alpha subunit.
Oryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neotele Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PWI2;
01-MAY-2000
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LLKQSSHCQEAGKRGRLEDASILCLDKEDDFLHVYYFFFKRTTSLILPGIIKAAAHVLYE
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                                                                                          FHFMFDKDMTILQFGNGIRRLMNRRD-FQGKPNFEEYFEILTPKINQTFSGIMTMLNMQF
                                                                                                                                                                                                       TEVEVSLMPPCFHNDCSEFVNQPYLLYSVHMKSTKP-SLSPSKPQSSLVIPTSLFCKTFP
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                                                                FHLILDQDLVLVQIGHGLRKRLTRKDGLRRSPTFQEHFSIVSPQIKCTFQGILTMLNTQF
                                                                                                                                                           TTVDVLKDPLTSKDSILQSSPQPSLLYTVVVKDAKTLSPSPLRATSAGTLPTSLFSTIFP
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Last annotation updat
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Pred. No. 2.8
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les 152;
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Neoteleostei;
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P79997;
01-MAY-1997
01-MAY-1997
01-MAR-2002
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SEQUENCE
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Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCc; 1.

SMART; SM00452; GUANYLATE_CYCLASES_1;

PROSITE; PS00452; GUANYLATE_CYCLASES_2;

PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Soluble guanylyl cyclase alpha subunit (EC 4.6.1.2).
Cryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mikami T.,
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HSSP; P19687; 1AWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-98237571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta subunits of soluble guanylyl cyclase
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Mikami T., Kusakabe T., Suzuki N.;
Molecular cloning of cDNAs and expression
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B000849; BAA19198.1; -.
                                                                                                                                                                                                                                                                                                                                                           Similarity
LLKQSSHCQEAGKRGRLEDASILCLDKEDDELHVYYFFFKRTTSLILPGIIKAAAHVLYE
                                                                                   DFEKTIAEQ----AVAAGVPVEVIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFST
                                                                                                                                                                                    QRKTSRSRVYLHTLAESICKLIFPEFERLNVALQR--TLAKHKIKESRKSL-----
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PEDIPGVCYFLES
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59.6%; Pred. No. 7e:
tive 101; Mismatches
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                                                                                        Query Match
Best Local S
Matches 406
                                                                                                                                                      Morinaga C., Yamamoto T., Moriya Y., Suzuki N.;

Morinaga C., Yamamoto T., Moriya Y., Suzuki N.;

I "Identification of tandem organization of soluble guanylyl cyclaphal and betal subunit genes in the Japanese pufferfish (Fugurbipes) genome.";

I submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB062171; BAB60907.1; -.

R EMBL; AB06218; BAB60907.1; -.

R EMBL; AB06219; BAB60905.1; -.

R InterPro; IPR001054; G_cyclase.

R Pfam; PF00311; guanylate_cyc; 1.

R PF031TE; PS00125; GUANYLATE_CYCLASES_1; UNKNOWN_1.

R PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

SEQUENCE 675 AA; 75498 MW; E71A283DC0369601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q90VV5 PRELIMINARY; PRT; 675 AA. Q90VV5; Q1-DEC-2001 (TrembLrel. 19, Created) 01-DEC-2001 (TrembLrel. 19, Last sequence up 01-JUN-2002 (TrembLrel. 21, Last annotation soluble guanylyl cyclase alphal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                      Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Morinaga C., Yamam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble guanylyl cyclase FRGCS-ALPHA1.
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                                                                                            Local Similarity
les 406; Conser
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VGVRMPRYCLFGNNVTLANKFESCSQPRKVNISPTTHRLVKGRPEFVFIPRSRQDLPANF
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                       MFCTKLKELKISGECPFTSSAKTNQL--
                                                      MFCTKLKDLKITGECPFSLLA-PGQVPNESSEEAAGSSESCKATVPICQDIPEKNIQESL
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illarity 60.1%;
Conservative 9
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Pred. No. 1.6e
6; Mismatches
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Soluble guannyly cyclase alpha-1 subunit.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glos
Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID-7130;
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   PROSITE;
                                    HSSP; P19687; IAWN.
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; 9uanylate_cyc; 1
SMART; SM00044; CYCc; 1.
                                                                                    J. Neurosci. 18:7244-725:
EMBL; AF062750; AAC61263
HSSP; P19687; 1AWN.
                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98409773; PubMed-9736646;
Nighorn A., Glbson N.J., Rivers D.N.
"The nitric oxide-comp pathway may
sensory afferents and projection ne
manduca sexta.";
                                                                                                                                           manduca sexta.
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                                                                                                                         18:7244-7255(1998).
GUANYLATE_CYCLASES_1;
GUANYLATE_CYCLASES_2;
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Glossata; Ditrysia;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update
01-MAR-2002 (TrEMBLrel. 20, Last annotation upda
GYCALPHA99B protein.
GYC-ALPHA-99B OR GYCALPHA99B OR DGCA1 OR CG1912.
                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                       Q24085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyase.
SEQUENCE
   SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                    647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 CPF-----SLLAPGQVPNESSEEAAGSSESCKATVPICQD-----IPEKNIQESLPQRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LWQGQVVQAKKFSNYTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HNALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA-GVPVEVIKESLGEEVFKICYEED---ENILGVVGGTLKDFLNSFSTLLKQSSHCQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPFRRASSQHQFANGGSSAPKKPEFRSRTSSVHLTGPEEEDGERNTLTLKHMSEAL-QLL
                                                                                                                                                                                                                                                                                                  FPKDIHGTCYFLHKYTHPGTDPGEP--QVKHIREALKDYGIGQANSTD
                                                                                                                                                                                                                                                                                                                  FPSEIPGICHFLDAY-QQGTN-SKPCFQKKDVEDGNANF-LGKASGID
                                                                                                                                                                                                                                                                                                                                                              VVGKTMLKYCLFGHNVTLANKFESGSEPLKINVSPTTYEWLIKFPGFDMEPRDRSCLPNS
                                                                                                                                                                                                                                                                                                                                                                                VVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPN
                                                                                                                                                                                                                                                                                                                                                                                                                          ETIGDAYCVASGLHRKVETHAPQIAMMALRMVETCAQHLTHEGNPIKMRIGLHTGTVLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         ETIGDAYCVAGGLHKESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMFCLKMPGSTALAEG--LEIKGQMVFCAESDSLLFVGSPFLDGLEGLTGRGLFISDIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVVRVRRWDNSVKKSSRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWHFITDKRLELVQLGAGFMRLFGTHLATHGSSLGTYFRLLRPRGVPLDFREILKRVNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-KRGRLE-DASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATDSVNTKDFMAKLGEVILLTAFSHNCRLERAFKCLGTNLTEFLTTLDS-VHDVLHDQDT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPSNECLHAAVTSLTKNQSDHYHKYN------CLRRLPDDVKTCRNYAYLQEIYDAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWIGEKIEAKSHDDVTMLFSDIVGFTSICATATPMMVIAMLEDLYSVFDIFCEELDVYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDATRDVILVGEQARAQDGLRRRMDKLKNSIEEASKAVDKEREKNVSLLHLIFPPHIAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNFEEYFEILTPK-INQTFSGIMTMLNMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SYTNDPRRF----RYEINAVPLHQKSKEDSCELVNEAASVATSTKVTDLKIGVASFCKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCFHNDCSEFVNQPYLLYSV--HMKSTK-----PSLSPSKPQSSLVIPTSLFCKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLKDETMEYEANFVCTTSQEGKIQLHLTTESEPVAYLLVGSLKAIAKRLYDTQTDIRLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699
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                                                                                                                                                                                                                       PRELIMINARY;
                                                               Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ξ
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Last annotation update)
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Pred. No. 2
                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                       676
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RA Adams N.D., Celniker S.E., Hil P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Glodek R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Dieywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Dieywam C.,
RA McKulov G., Milshina N.F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Melson D.R., Nelson K.A., Mobarty C., Morris J., Moshrefi A.,
RA Mchilov G., Milshina N.F., Karper G.H., K., Scheeler F., Shen H.,
RA Keinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Keinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Klamos I., Simpson M., Strong R., Backeb M.,
RA Shue B.C., Siden Klamos I., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Stapleton M., Susyski M.P., Esce M.G.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Shou S., Zhao Q., Zheng L.,
Ra Shobs R.A., Myers E.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
The General String S., Shen H., Schen G. S., Shen H., Schen G., Shen H., Schen G., Shen G., 
                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain soluble guanylyl cyclase.";
J. Biol. Chem. 270:15368-1376(1995).
EMBL; AE003770; AAP56917.1; -.
EMBL; U27117; AAAB7940.1; -.
HSSP; P19687; 1AWN.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00211; guanylate_cyc;
SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0013972; Gyc-alpha-99B
InterPro; IPR001054; G_cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shah
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MEDLINE=95318108; PubMed=7797526;
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
SEQUENCE 676 AA; 75662 MW; CE8097E1EC3787F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two Drosophila genes that encode the brain soluble guanylyl cyclase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Hyde D.R.;
    142
                                         160 KDFLNSFS---TLLKQSSHCQEAGKRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILP
                                                                                    87
                                                                                                                                                                      27
                                                                                                                                                                                                                                                                            Similarity
QEFLGSLDGVYDVLK----LQEED----VTDTGFVCAGEGE----LIFTSERPVIAWLLL
                                                                                                                         KSLEREDFEKTIAE-----QAVAAGVPVEVIKESLGEEVFKICYEE-DENILGVVGGTL
                                                                                                                                                                                                           SLPQRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAK-----HKIK---ESR
                                                                                  KSCANYDYLADIQELLLKMDEASASEILV----
                                                                                                                                                                  ALEDEELSDDALTLTHLQMAIQLLTAPSNEDLNTAVTSLVAKYRQNWPNIHKLKLDPQTF
                                                                                                                                                                                                                                                    Conservative 117;
                                                                                                                                                                                                                                                                          27.6%;
37.8%;
                                                                                                                                                                                                                                                                        Score 991.5;
Pred. No. 4.4
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                          No. 4.4e-69;
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                                                                                                                                                                                                                                                                                           Length
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417 432

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RESULT 10
Q95SQ4
ID Q95SQ
AC Q95SQ
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT CHAR
DE GNC-#
OS Dross
GN GYC-#
OS Pterly
OC Ephyy
OC Ephy
OC Ephyy
OC Ep
                                                                                                                                                                                           Query Match
Best Local S
Matches 246
                                                                                                                                                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY060654; AALZ8202.1; -.

EMBL; AY060654; AALZ8202.1; -.

FlyBase; FBgn0013972; Gyc-alpha-99B.
InterPro; IPR001054; G_Cyclase.
Pfam; PF00211; guanylate_cyc; 1.

PROSITE; PS50125; GGANYLAFE_CYCLASES_2; 1.

SEQUENCE 676 AA; 75658 MW; CB9183E1EC314138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BERKELEY;
Stapleton "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q95SQ4
Q95SQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYC-ALPHA-99B OR GYCALPHA99B OR CG1912.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; H.
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418
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                               107
                                                                                     27
                                                                                                                                        58
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALKINVSPTTKDWLTKHEGFEFELQPRDPSFLPKEFPN--PGGTETCYFLESFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRKINVSPTTYRLLKDCPGFVF--TPRSREELPPNFPSEIPG---ICHFLDAYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALKMIDACSKHITHDGEQIKMRIGLHTGTVLAGVVGRKMPRYCLFGHSVTIANKFESGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADFGCQATTYFDFKRPKGLTMKFRDIVRRTYTPFLIGLNNPPGAVDFPAIGLEIKGQMVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PETVQRSNSSNASDLQMNSSSFCKMFPWHFIMNEQLELVQLGRGFSKLY-----KPYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSLKALTRMLYKVDVNIKIEP--VEGDARRY---RYLFSLVKDNSQTMLMGRPTSVSKTI 244
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        KSLEREDFEKTIAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQ-----SSLVIPTSLFCKTFPFHFMFDKDMTTLQFGNGIRRLMNRRDFQGKPNF
                                                                                     ALEDEELSDDALTLTHLQMAIQLLTAPSNEDLNTAVTSLVAKYRQNWPNIHKLKLDPQTF
                                                                                                                                        SLPQRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAK-----HKIK---ESR
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFEILTPK-INQTFSGIMTMLNMQFVVRVRRWDNSVKKSSRVMDLKGQMIY
                                                                                                                                                                                                                           27.48;
37.68;
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19,
20,
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Last sequence update)
Last annotation updat
                                                                                                                                                                                           Score 985.5;
Pred. No. 1.3e
17; Mismatches
                                                                                                                                                                                                                                                                                               _CYCLASES_2; 1.
W; CB9183E1EC314138 CRC64;
  -QAVAAGVPVEVIKESLGEEEVFKICYEE-DENILGVVGGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                        e 985.5; DB 5;
. No. 1.3e-68;
ismatches 210;
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; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                              Indels
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                                                                                                                                                                                           Query Match
Best Local S
Matches 162
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Q1.-JUN-2002 (TrEMBLrel. 21, Created)
Q1.-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1.-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1.-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Soluble guanylate cyclase alpha2d (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of a novel variant of the cyclase beta2 subunit."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ EMBL; AB079780; BAB84824.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8R5L4
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )kamoto H., Asakawa T.
'Molecular cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
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                                                                               PRKINVSPTTYRLLKDCPGFVF--TPRSREELPPNFPSEIPG---ICHFLDAYQ
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                            ALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKINVSPTPKDWLTKHEGFEFELQPRDPSFLPKEFPN--PGGTETCYFLESFR
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220
Conservative
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                                                                                                                                                                                                                                                                                               220
24646 MW;
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                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                           Score 823; DB 11;
Pred. No. 1.5e-56;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vert
Sciurognathi;
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220
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649

612

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552 477 492

537

databases

soluble

Euteleostomi; ; Murinae; Rat

Rattus.

CRC64;

Length Indels

220; 48;

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alphal and betal subunit genes in the Japanese pufferfis rubripes) genome.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062172; BAB60908.1;
EMBL; AB062170; BAB60908.1;
InterPro; IPR001054; G_cyclase.
InterPro; IPR001034; Zn_carbOpept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00211; guanylate_cyc; 1.
PROSITE; PS00132; CARBOXXPEPT_ZN_1; UNKNOWN_1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
SEQUENCE 617 AA; 70236 MW; 7B531B5896A06191 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TEMBLE). 19, Created)
01-DEC-2001 (TEMBLE). 19, Last sequence up
01-MAR-2002 (TEMBLE). 20, Last annotation
Soluble guanylyl cyclase betal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morinaga C., Yamamoto T.,
"Identification of tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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QMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKR
                                                                                                                                                                                                                                                                                      TSLILPGIIKAAAHVLYETEVEVSLMPP----CFHNDCSEFVNQPYLLYSVHMKSTK---
                                                                                                                                                   FYEDLDGFEENGTQETRISPYT-FCKAFPFHLMFDRDLMLTQCGNAIYRVLPQLQ-PGSC
                                                                                                                                                                                                                                                                                                                                    LRVLGSNVREFLQNLDAL-----
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                                                                 ILPSVFSLVRPHIDFSFHGILSHINTVFVLRSKEGLLNVETVENEDELTGVEISCLRLKG
                                                                                                          NFEEYFEILTPKINQTFSGIMTMLNMQFVVR-----VRRWDNSVKKSSRVMDLKG
                                                                                                                                                                                                                                             LQDIVIGITKTVAQQIHGTETEMKMIQPKSKECDH-----IKFLIEEKDSEEEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVRMPRYCLFGNNVTLASKFESGSHPR
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                                                                                                                                                                            -PSLSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKP
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n organization of soluble guanylyl cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 788; DB 13;
Pred. No. 3.5e-53;
2; Mismatches 217;
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Best Local 9
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077106;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nighorn A., Gibson N.J., Rivers D.M., Hildeb
"The nitric oxide-cGMP pathway may mediate c
sensory afferents and projection neurons in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Soluble guanyly1 cyclase beta-1 subunit.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID-7130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Neurosci. 18:7244-7255(1998).
EMBL; AF062751; AAC61264.1; -.
HSSP; P16068; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-98409773; PubMed-9736646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         manduca sexta."
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  228
                                           299
                                                                                                                                 248
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                                                                                                                                                                                                                                                                                    131 VIKESLGEEVFKICYEED-ENILGVVGGTLKDFLNSFSTLLKQSSHCQEAGKRGRLEDAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         196;
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VQAGRTVSRLLPRVTRPG-CKITDVLDTVRPHLEMTFANVLAHINTVYVLKTKPEEMSVT
                                        LQFGNGIRRLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSV-
                                                                   ITETSTTGRVSAPEIA-EIETLSLEPKVSP--
                                                                                                                                                                         FRCTERPEDGALVLHYYSDRPGLEHIVIGIVKTVASKLHNTEVKVEILKTKEECDHVQFL
                                                                                                                                                                                              ILCLDK-EDDFLHVYYFFFKRTTSLILPGIIKAAAHVLYETEVEVSLMPPCFHNDCSEF-
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                                                                                                                          ------VNQPYLLYSVHMKSTKPSLSPSKPQSSLVIPTSLECKTEPEHFMFDKDMTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 AA; 68099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 785.5;
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59;

Gaps

13;

189 64 130

298

227

179

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RESULT 14
Q91XJ7
ID Q91XXJ
AC Q91XJ
AC Q91XJ
DT 01-DE
DT 01-DE
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DT 01-MA
DE SOLUL
GN GUCYI
OS RATTL
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Best Local S
Matches 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY; MEDLINE-21391941; PubMed-11406623; Koglin M., Vehse K., Budaeus L., Scho
                                                                                                                                                                                                                                                                                                                              InterPro; IPR001054; G_Cyclase.
InterPro; IPR001230; Prenyl_site.
Pfam; PF0021; guanylate_cyc; 1.
PR0SITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
PROSITE; PS00152; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS00154; PRENYLATION; UNKNOWN_1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-MAR-2002 (TrEMBLrel. 20, La
Soluble guanylyl cyclase beta
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n the Absence of a Second Subunit.";
Biol. Chem. 276:30737-30743(2001).
MBL; AY004153; AAR86581.1;
nterpro: IPRONICE.
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                                                                                                                                                HSYLALSYQEMNAPSFRVEEGADGAMLLHYYSDRHGLCHIVPGIIEAVAKDFFDTDVAMS
                                                                                                                                                                  KLIQEACKVLDVSMEAILKLFGEYFFKFCKMSGYDRMLRTLGGNLTEFIENLDAL----
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FMFDKDMT1LQFGNGTRLMNRRDFQGKPNFEEYFE1LTPK1NQTFSG1MTMLNMQFVVR
                            LRMKERYLNIPVCPGEKSHSTAVRASVLFGKGPLRDTFQPVYPERLWVEEEVFCDAFPFH
                                                                                       IL-----DMNEEVERTGKKEHVVFLVVQKAHRQIRGAKASRPQGSEDSQADQEALQGTL
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Last annotation updat
ta 2 subunit.
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Pred. No. 8.
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# Murinae; Rat
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Best Local Similarity
Matches 200; Conserv
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Eukaryota; Metazoa; C
Mamumalia; Eutheria; R
NCBI_TaxID=10090;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Soluble guanylate cyclase beta-1 subunit.
GUCY1B3 OR GC-S-BETA-1.
                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                     "Genomic organization of alpha soluble guanylyl cyclase genes. Proc. Natl. Acad. Sci. U.S.A. 9 EMBL; AF020339; AAB94875.1; ---
EMBL; AF297083; AAG17447.1; ---
HSSP; P16068; IAWN.
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                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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rPro; IPR001054; G_cyclase.
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                    VVGGTLKDFLNSFSTLLKQSSHCQEAGKRGRLEDASILCLDKE-DDFLHVYYFFPKRTTS
                                                              KIKESRKSLEREDFEKTIAEQAVAAGVPV-----EVIKESLGEEVFKICYEED-ENILG
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GUANYLATE_CYCLASES_2;
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Rodentia;
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                                                                                    Score 781.5; I
Pred. No. 1.1e-
97; Mismatches
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EMBL/GenBank/DDBJ
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HDHLATIYPGMRAPSFRCTDAEKGKGLILHYYSEREGLQ
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ANKESUSVPKK.NVSPTITKIL 626 :: :		THAVOIALMALKMMELSDEVMSPHGEBIKMRIGLHSGSVFAGVVGVKMBRVGLEGNMVT. 603	ILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGF 430 TAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESD 543	KLKATLEQAHQALEEKKKTYDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGF 490	TYLPEADSILFICSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEQFREEYKLTQELE 370	IYIVESSAILFIGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKRLG 430	LSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGAEISCLRLKGOM 310	EEYFEILIPKINGTESGIMTMLNMQFVVRVRRWDNSVKKSSRVMDLKGQM 370	EDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRNLVVTQCGNAIYRVLPQLQ-PGNCSL 250	LSPSKPQSSLVIPTSLECKTPPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNF 320	DIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFLIEEKESKEEDFY 192	LILPGIIKAAAHVLYETEVEVSLMPPCFHNDCSEFVNQPYLLYSVHMKSTKPS 265

Search completed: June 27, 2003, 13:04:41 Job time: 38.7899 secs

Title: Perfect score: Sequence:

US-09-762-767A-2 3593 1 MFCTKLKDLKITGE

MFCTKLKDLKITGECPFSLL.....

protein

protein search, using sw model

Copyright

June

27,

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,

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Total number

of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

178, App 178, App 174, App 174, App 174, App 174, App 174, App 175, App 175, App 175, App 125, App 126, App 127, App 128, App 129, App 129, App 129, App 129, App

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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; APPLICANT: Garbers, David L.; APPLICANT: Schulz, Stephanie; TITLE OF INVENTION: CLONING THE E; NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-623-033-2
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US-07-623-033-2
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Matches 98
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/623,033
FILING DATE: 19901206
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REGISTRATION NUMBER: 30,955
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1075 amino aci
TYPE: AMINO ACID
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REGISTRATION NUMBER: VU90
REFERENCE/DOCKET NUMBER: VU90
TELECOMMUNICATION INFORMATION:
"""" TO NO: 2:
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MEDIUM TYPE: Floppy disk
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STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606-4002
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STREET: 10
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                                                                                                      423 DGLKKRL----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFS
                      479 NVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL
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                                                                               DTLIRRLQLYSRNLEHLVEERTQLYKAERDRADHLNFMLLPRLVVKSLKEKGIVEPELYE
EVTIYESDIVGETTICKYSTPMEVVDMLNDIYKSFDQIVDHHDVYKVETIGDAYVVASGL
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                                                                                                                                                                                                                                                                                                                         1075 amino acids
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US-09-324-542-178
US-09-205-426-178
US-08-997-080-174
US-08-997-362-174
US-09-095-855-174
US-09-324-542-174
US-09-324-542-174
US-09-325-426-174
US-08-857-076-75
US-08-857-076-75
US-08-997-080-125
US-08-997-852-125
US-09-925-855-125
US-09-925-855-125
US-09-324-542-125
US-09-324-542-125
US-09-326-125
US-09-326-125-126-125
US-09-326-125-126-125
                                                                                                                                                            Score 407.5;
Pred. No. 3.1e
47; Mismatches
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; ORGANISM: Homo sapiens
US-09-412-210-1
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US-09-412-210-1
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                                                                                                                     Sequence 8, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
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TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
FILE REFERENCE: 5800-47
CURRENT APPLICATION NUMBER: US/09/412,210
CURRENT FILLING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                      APPLICANT: Tang, Wei
APPLICANT: Gilman, A
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                         CORRESPONDENCE ADDRESS:
                                       NUMBER OF SEQUENCES:
           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                  GSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDC------
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                                                  Gliman, Alfred G.
VENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
VENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                         Tang, Wei-Jen
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          Arnold,
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        White &
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Pred. No. 4.6e-23;
55; Mismatches 98;
        Durkee
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US-08-726-214-14
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                                                                                                                                                                         Sequence 14, Applicat Patent No. 6107076 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                        APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: PatentIn Release #1.0, CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewit!
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     COUNTRY:
                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                               4, Application US/08726214 6107076
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                  Texas
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                                                  P.O. Box 4433
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United States of
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                                                                Arnold,
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SYSTEM: PC-DOS/MS-DOS
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31.2%;
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Pred. No. 1e-22;
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                                                                                                                             ADENYLYL CYCLASE
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RESULT 5
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                                                                                                              GENERAL INFORMATION:
APPLICANT: LYENGAI, SLINIVAS RAVI
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILE REFERENCE: 29770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                            Sequence 3, Application US/08307896C Patent No. 6034071
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                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 1099 amino acids
                                                                        CURRENT APPLICATION NUMBER: US/08/307,896C CURRENT FILING DATE: 1994-09-16
                                    NUMBER OF SEQ
SOFTWARE: Fast
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APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37.642
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/726,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 ANAVILLGG-----NFTGA---FHKHQLQDASRDLFIY--------
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  1090
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                                    SEQ ID NOS: 9
FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                IDPRSQQPPPPS 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.9%; Score 319.5; llarity 26.3%; Pred. No. 1.9. Conservative 64; Mismatches
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ches 95;
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                                                                                    TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                   APPLICATION NUMBER: US 6
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                    TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewit
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                      NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                 STRANDEDNESS:
                                                                                                                    TELEPHONE:
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POPOLOGY:
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                              amino acid
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                                                                                                    (512)
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                                                                                                  (512) 418-3000
512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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                                                                                                                                                    UTSD:450
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                                                                                                                                                                                                                                                                                             Herewith
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Score 319;

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Length 1090;

Best Local Similarity

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; MOLECULE TYPE:
PCT-US95-11808-3
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Query Match 8.9%; Street Local Similarity 30.4%; Properties 80; Conservative 53;
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino aci
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S.
REGISTRATION NUMBER: 26,1
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1180
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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STATE:
                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 30 Roc
CITY: New York
                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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10112-0228
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                                                                                                                             1090 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 Rockefeller Plaza
                                                                                                                                                                                              : (212) 408-2500
(212) 765-2519
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CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
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MUTANT ACTIVATED GSALPHA AND
                                                                                                                                                                                                                                                                                                                        US 08/307,896
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                Score 319; DB 5;
Pred. No. 2.1e-22;
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                                                                                                                                                                                                                                            29970 165/28755
   Mismatches
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 86;
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Gaps
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                                                                                                                                            TOPOLOGY:
US-08-726-214-6
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                                                                                        Query Match
Best Local :
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                                                                          Matches
                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
APPLICANT: Gilman, Alfred G.
APPLICANT: GILMAN, ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: 77210
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                  NAME: Highlander, St
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/005,498 FILING DATE: 04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                              LENGTH:
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433 KATLE-----QAHQALEEEKKKTVDLLCSIFPCEVAQQL-------WQGQVVQA 474
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                                                                                                                                                                                                                                                                                  (512) 418-3000
                                                                                                                                                                                                                                                                  474-7577
                                                                     8.4%; Score 303; DB 3; 30.7%; Pred. No. 8.8e-21; ative 50; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                  Steven L
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                                                                                                       Length 1144;
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US-08-726-214-2
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                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (512) 418-3000
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APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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251 CIEDRLRLEDENEKQERLLMSLLPRNVAMEMKEDFLKPPERIFHKIYIQRHDNVSILFAD 310
                                                    436 LEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQG------QVVQAKKFSNVTMLFSD 486
                                                                                                                                                           376 SSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKRLGKLKAT 435
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                         8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,642
                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                Score 302; DB 3; 1
Pred. No. 1.1e-20;
7; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UTSD:450
                                                                                                         ---VNVYGIF--VRILAERAQRKAFLQAR-----N 250
                                                                                                                                                                                                                                                                  Length 1134;
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US-08-726-214:18
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewit CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/005,498 FILING DATE: 04-OCT-1995
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                                                                                                                                          494 CSQCSPLQVIIMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIALMA 553
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                                                  554 LKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLEGNNVTLANKFESCSVP 613
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                                                                                                    ASQCTAQELVKLLNELFGKFDELATENHCRRIKILGDCYYCVSGLTQPKTDHAHCCVEMG 142
                                                                                                                                                                                                                                                               LEEEKKKTVDLLCSIFPCEVAQQLWQG-----QVVQAKKFSNVTMLFSDIVGFTAI 493
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                                                                                                                                                                                                                                                                                                                 8.3%; Score 299.5; DB 3; 32.6%; Pred. No. 5.5e-21; tive 44; Mismatches 77;
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US-08-726-214-16
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-08-864-785-2
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Patent No. 6107076
GENERAL INFORMATION:
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Best Local
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SOFTWARE: FastSEQ for
SEQ ID NO 2
LENGTH: 1253
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APPLICANT: Kaplan, Joshua
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CURRENT APPLICATION NUMBER: US/08/864,785A
CURRENT FILING DATE: 1997-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oppenheimer, Allison
APPLICANT: Hart, Anne C.
                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE |
TITLE OF INVENTION: AND USES
NUMBER OF SEQUENCES: 31
                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewit CLASSIFICATION: 435
                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                          United States of America
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                 Concurrently Herewith
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30.5%;
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Pred. No. 3.0
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RESULT 13 US-08-726-214-10

Sequence 10, Application Patent No. 6107076 GENERAL INFORMATION:

US/08726214

APPLICANT:

Wei-Jen

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TOPOLOGY:
US-08-726-214-16
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Best Local Similarity 22.5%;
Matches 147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 6
FILING DATE: 04-OCT-1995
ATTORNEY AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: UTSD:450
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                  VVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPR 637
VIGAKKPQYDIWGKTVNLASRMDSTGVSGRIQVPEETYLILKD-QGFAFDYR 1147
                                                                                                                                                                         NVTMLFSDIVGFTAICSQC----SPLQVITMLNALYTRFDQQCGE---LDVYKVETIGDA 531
                                                                                                                                                                                                             EYTARLDFLWRVQAKEEINEMKDLREHNENMLRNILPGHVARHFLEKDRDNEELYSQSYD
                                                                                                                                                                                                                                            KLKATLE-----QAHQALEEEK---KKTVDLLCSIFPCEVAQQLWQ-----GQVVQAKKFS
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                                                                    YMAVSGLSPEKQQCEDKWGHLCALADFSLALTESIQEINKHSFNNFELRIGISHGSVVAG
                                                                                                     YCVAGGLHKESDT-----HAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAG 585
                                                                                                                                         AVGVMFASIPGFADFYSQTEMNNQGVECLRLLNEIIADFDELLGEDRFQDIEKIKTIGST 1036
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Pred. No. 7e-
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RESULT 14
US-09-008-097-4
US-09-008-097-4
; Sequence 4, Application US/09008097
; Patent No. 6306330
; GENERAL INFORMATION:
Hammond, H. Kirk
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Best Local 9
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino aci
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gilman, TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/005,498 FILING DATE: 04-OCT-1995
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1 Similarity 26.4%;
83; Conservative 5
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                                                                                                                                                ANPEDEVDEFLGRA 560
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                                                                                                                                                                                                             IAKMNRQRTNSIGHNPPHWGAERPFYNHL---
                                                                                                                                                                                                                                                                             EAGGKAGRIHITKATLNYLNGDYEVEPGCGGERNAYLKEHSIETFLILRCTQKRKEEKAM
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SOLUBLE MAMMALIAN ADENYLYL CYCLASE
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Pred. No. 7.1e-19;
52; Mismatches 108;
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                                                                                                          RESULT 15
US-09-008-097-6
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                                                       Sequence 6, Application US/09008097 Patent No. 6306830 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:

Hammond, H. Kirk Insel, Paul A. Ping, Peipei

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US-09-008-097-4
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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APPLICATION NUMBER: US
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NAME: Dylan, Tyler M
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SOFTWARE: FastSEQ for Windows Version
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ZIP: 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                               609
                                                                                                                        175 GFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGDCYYCVSGLPEARADHAHC
                                                                                                                                                      489 GFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQ 548
                                                                                                                                                                                     115 QARLHLQHENRQQERLLLSVLPQHVAMEMKEDINTKKEDMFHKIYIQKHDNVSILFADIE 174
 295
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                                                                                                                                                                                                                                                                                                                                                                                          I: 604 amino acids amino acid
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                           SCSVPRKINVSPTTYRLL 626
                                                                                         IALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFE 608
                                                            CVEMGVDMIEAISLVREVTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHME
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AGSRAGRIHITRATLQYL 312
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Gao, Meihua
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                                                                                                                                                                                                                                                                Score 282.5;
Pred. No. 3.
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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
; FRAGMENT TYPE: inter
US-09-008-097-6
Search completed: June 27, 2003, 13:05:57 Job time: 16.2322 secs
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NAME: Dylan, Tyler M
REGISTRATION NUMBER: 2200
REFERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEPAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
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Best Local Similarity
Matches 63; Conserv
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CTIY: PALO ALTO
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APPLICATION NUMBER: US,
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APPLICATION NUMBER:
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ZIP: 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                       609
                                                                                                                                                      446 CVEMGVDMIEAISLVREVTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHME 505
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                                                                             506 AGSRAGRIHITRATLQYL 523
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                                                                                                                   SCSVPRKINVSPTTYRLL 626
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internal
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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3593
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA: *
             /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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                                                                                                                                                                                                              /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	BB	ID	Description
-	3593	100.0	1	ص	US-10-205-823-162	Sequence 162, App
N	3265.5	90.9		9	US-09-952-213D-2	Sequence 2, Appli
ω	408.5	11.4		9	US-10-157-031-18	Sequence 18, Appl
4	408.5	11.4		10	US-09-819-249-2	Sequence 2, Appli
σı	325.5	9.1	1077	9	US-10-121-911-1	Sequence 1, Appli
σ	316	8.8		9	US-10-282-942-2	Sequence 2, Appli
7	303.5	8.4		10	US-09-925-297-811	Sequence 811, App
8	282.5	7.9		10	US-09-750-240-4	Sequence 4, Appli
9	282.5	7.9		10) US-09-750-240-6	Sequence 6, Appli
5	280.5	7.8		ø	US-10-175-158-2	Sequence 2, Appli
Ξ	279.5	7.8		9	US-10-201-000-2	Sequence 2, Appli
2	279.5	7.8		10) US-09-750-240-11	Sequence 11, Appl
ü	278	7.7		10) US-09-750-240-13	Sequence 13, Appl
4	263.5	7.3		12	0S-10-071-223-2	Sequence 2, Appli
5	260.5	7.3		10) US-09-751-100B-2	Sequence 2, Appli
16	260.5	7.3		12	2 US-10-071-223-3	Sequence 3, Appli
17	255.5	7.1		10) US-09-751-100B-99	Sequence 99, Appl
18	212	5.9		9	US-09-989-442-95	Sequence 95, Appl
19	207	л 20		٥	TS-09-761-868-791	Seguence 70/ Ann

195 5.4 670 9 US-10-051-643-178 195 5.4 670 9 US-09-880-505-178 195 5.4 722 9 US-09-880-505-174 195 5.4 722 9 US-09-880-505-174 195 5.4 107 10 US-09-884-353A-76 192.5 5.4 107 10 US-09-844-353A-76 193 5.3 112 10 US-09-80-505-125 187 5.2 419 9 US-09-80-505-125 187 5.2 419 9 US-09-804-353A-75 188 4.1 109 9 US-09-989-442-92 148 4.1 109 9 US-09-989-442-143 148 4.1 109 9 US-09-764-868-795 148 4.1 109 9 US-09-764-868-1060 148 4.1 109 9 US-09-764-868-1060 148 4.1 109 9 US-09-751-100B-60 137.5 3.8 85 10 US-09-751-100B-61 133.5 3.7 85 10 US-09-751-100B-56
44 722 9 U U 4 722 9 U U 4 722 9 U U 4 722 9 U U 5 72 72 9 U U 5 72 72 9 U U 6 72 72 9 U U 6 72 72 72 9 U U 6 72 72 72 9 U U 7 7 7 7 8 8 5 10 U 7 7 8 8 5 10 U 7 7 8 8 5 10 U 7 7 8 5 10 U
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US-10-651-643-178 US-09-880-505-178 US-09-880-505-174 US-09-880-505-174 US-09-915-582-50 US-09-9205-658-76 US-09-9205-658-76 US-09-844-353A-75 US-09-844-353A-75 US-09-880-505-125 US-09-880-505-125 US-09-989-442-92 US-09-989-442-92 US-09-989-442-143 US-09-989-442-1660 US-09-751-1008-60 US-09-751-1008-61 US-09-751-1008-55 US-09-751-1008-55 US-09-751-1008-56

ALIGNMENTS

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US-10-205-823-162
; Sequence 162, Application US/10205823
; Publication No. US20030108963A1
                                                                  ; ORGANISM: Homo sapiens US-10-205-823-162
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                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2002-03-05
                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 162
LENGTH: 690
TYPE: PRT
Query Match
Best Local Similarity
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TITLE OF INVENTION:
                                                                                                                                                                                                 NUMBER OF SEQ
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INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
INVENTION: METHODS FOR IDENTIFICATION, ASSI
INVENTION: THERAPY OF PROSTATE CANCER
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Zhao, Xumei
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Kamatkar, Shubhangi
Wonsey, Angela M.
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Gorbatcheva, Bella
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Endege, Wilson O.
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100.0%;
Score 3593; DB 9; Pred. No. 1e-305;
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                      Length 690;
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                                                                                                     Sequence 2, Application US/09952213D Publication No. US20030096240A1
GEMERAL INFOCMATION:
APPLICANT: MURAD, FERID
APPLICANT: SHARIMA, IRAIDA G.
APPLICANT: KRUENACKER, J. S.
APPLICANT: MARTIN, E.
TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE
                   TYPE: PRT
ORGANISM: Mus |
S-09-952-213D-2
 Query Match
                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                    CURRENT APPLICATION NUMBER: US/09/952,213D CURRENT FILING DATE: 2002-08-16 NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                               FILE REFERENCE: UTSH: 252US
                                              LENGTH: 691
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; TYPE: PRT
; ORGANISM: Homo
US-10-157-031-18
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US-10-157-031-18
; Sequence 18, Application US/101
; Publication No. US20030108890A1
; GENERAL INFORMATION:
                                                                                                 SEQ ID NO 18
LENGTH: 1073
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                                                                FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                        APPLICANT: Baranova, A. V. APPLICANT: Yankovsky, N.
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Kozlov, A. P.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-249-2
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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Best Local Similarity
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Best Local (
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CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/192,229
PRIOR FILING DATE: 2000-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer Cel
TITLE OF INVENTION: Alimentary Canal Origin
FILE REFERENCE: TJU2412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Waldman, Scott A. APPLICANT: Park, Jason APPLICANT: Schulz, Stephani
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                                                                                                                                                                                                                                                            EVTIYFSDIVGFTTICKYSTPMEVVDMLNDIYKSFDHIVDHHDVYKVETIGDAYMVASGL
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                                                           FL----DAYQQGTNSKPCFQKKDVEDGNAN 681
                                                                                                    LFGDTVNTASRMESTGLPLRIHVSGSTIAILK---
                        FLYEVRGETYLKGRGNETTYWLTGMKDQKFN 1009
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Pred. No. 1.2e-26;
Prematches 92;
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Pred. No. 1.2e-26;
Pred. No. 1.2e-26;
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                                                           ; TYPE: PRT
; ORGANISM: HOMO
US-10-282-942-2
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Patent No. US20020164632A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 21529, A NOVEL ADENVLATE CYCLASE
FILE REFERENCE: 5800-47
CHERRY OF THE REFERENCE: 5800-47
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LENGTH: 1077
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local (
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Query Match
Best Local Similarity
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CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 60/335,047
PRIOR FILING DATE: 2001-10-31
                                                                                                                                                                                                                                                                        APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS
FILE REFERENCE: MPIO1-240P1RM
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                                                                                                                    LENGTH: 1080
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    316; DB 9;
No. 1.5e-18;
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                  Length 1080;
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; NAME/KEY: SITE ; LOCATION: (829) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-09-925-297-811
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Best Local 9
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SEQ ID NO 811
LENGTH: 855
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE LOCATION: (479) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                      AGGLHKESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRY 594
                                                                                                                                                                                                                          KKESNYTMLESDIYGETAICSQCSPLQVITMLNALYTREDQQCGELDVYKVETIGDAYCV 534
                                           DVWSTDVTVANKMEAGGIPGRVHISQST----MDC----
                                                                                CLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPG--
                                                                                                                     ICGLPDYREDHAVCSILMGLAMVEAISYVREKTKTGVDMRVGVHTGTVLGGVLGQKRWQY 186
                                                                                                                                                                                                 YRHENVSILFADIVGFTQLSSACSAQELVKLLNELFARFDKLAAKYHQLRIKILGDCYYC 126
                                                                                                                                                                                                                                                                             KAFLEARQSLEVKMNLEEQSQQQENLMLSILPKHVADEMLKDMKKDESQKDQQQFNTMYM 66
                                                                                                                                                                                                                                                                                                                  KATLE-----QAHQALEEEKKKTVDLLCSIFPCEVAQQL-------WQGQVVQA 474
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Pred. No. 1.3e-17;
2; Mismatches 93;
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    -SKPCFQKKDVEDG
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SEQ ID NO 4
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-750-240-4
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Best Local
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                                                                                              APPLICANT:
                                   TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART TITLE OF INVENTION: FAILURE FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240 CURRENT FILING DATE: 2001-10-12
                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
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                                                                                                                                       APPLICANT:
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                                                                                                                                                                        APPLICANT: Hammon, H. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1996-09-05
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Local Similarity 31.8%;
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Post, S. R.
                                                                                                                                                        Insel,
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Pred. No. 5.3e-16;
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                                                                                                                       TYPE: PRT; ORGANISM: human type V adenylyl cyclase US-10-175-158-2
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PRIOR FILLING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILLING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR FILLING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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                                       Query Match
Best Local Similarity 26.4:
                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10175158 Publication No. US20030008371A1
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Best Local Similarity 31.8%;
Matches 63; Conservative 4
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tomlinson, James
APPLICANT: Cor Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5027-01-US
CURRENT FAPLLCATION NUMBER: US/10/175,158
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US/09/473,716
PRIOR APPLICATION NUMBER: US/09/473,716
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US98/13540
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,901
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/886,362 PRIOR FILING DATE: 1997-07-01
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ORGANISM: Homo sapiens
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549 IALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFE 608
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                                                    7.8%; Score 280.5; DB 9; 26.4%; Pred. No. 2.4e-15; tive 52; Mismatches 108;
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; TYPE: PRT ; ORGANISM: human type VI adenylyl cyclase US-10-201-000-2
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SOFTWARE: PatentIn Ve:
SEQ ID NO 2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/474,076
PRIOR FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: PCT/US98/13694
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,904
PRIOR FILING DATE: 1997-07-01
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TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tomlinson, James E. APPLICANT: COR Therapeutics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 44481-5028-01-US
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498
                                               600 NYTLANKFESCSVPRKINVSPTTYRLL
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DVTLANHMEAGGRAGRIHITRATLQYL
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Sequence 11, Application Upatent No. US20020103147A1

Application US/09750240

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US-09-750-240-13
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Matches 63; Conserv
                FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-77
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
                                                                                                                                                        APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: FAILURE
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PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
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CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
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TYPE: PRT
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APPLICATION NUMBER: US 08/924,757
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                                                                                                                                                                                                 Ping, P.
Post, S. R.
Gao, M.
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                                                                                                                         ; TYPE: PRT
; ORGANISM: human type IX adenylyl cyclase
US-10-071-223-2
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US-10-071-223-2
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                           SEQ ID NO 2
                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/098,559
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/473,717 PRIOR FILING DATE: 1999-12-29
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/071,223
CURRENT FILING DATE: 2002-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COR Therapeutics, Inc.
APPLICANT: University of Washington
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-07-01
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1997-06-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/886,440
INFORMATION:
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                                                                          7.3%;
29.9%;
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                                                         58;
                                                   Score 263.5; DB 1
Pred. No. 7.7e-14;
8; Mismatches 89
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                                                                                          DB 12;
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CURRENT APPLICATION NUMBER: US/09/751,100B
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1353
TYPE: PRT
ORGANISM: Mouse
US-09-751-100B-2
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Best Local Similarity 29.4*
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Patent No. US20020142436A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor
FILE REFERENCE: P27948A
                                                                                                                                                                                                            578
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AAW30601 AAW88525 AAR99251 AAR99250	ABB64494 ABB6567	AAB83939 ABGG3067 AAG67400 AAW88524 AABE17133	AAW37371 AAU08788 ABB72034 AAR38861 AAB83941 AAB83940	AAR1 0399 ABB71674 ABB59684 ABB561743 ABB64661 AAW32063	AAG00754 AAG11280 AAG11281 AAG11281 ABB11783 AAR38862 ABB71206 AAR10867 AAR38867
Human type IX aden Adenyl cyclase typ Murine adenylate c Type V adenylyl cy	21 ~~ ~	Amino acid sequenc Novel human diagno Partial amino acid Adenyl cyclase-1 (Human adenylyl and	Human ST receptor Human guanylin cyc Drosophila melanog GC-C. Rattus ratt Amino acid sequenc Amino acid sequenc	סססס	Human secreted pro Human atrionatriur Human atrionatriur Human ARIO-A recept GC-A. Rattus ratt Drosophila melanog NRB(Pr0555, Glu65

ALIGNMENTS

RESULT 1 AAY51608 Human; guanylyloyclase alphai; hsGCalphai; hsGCbetai; soluble; guanylyloyclase betai; antiarteriosclerotic; vasotropic; hypotensive; gene therapy; arteriosclerosis; restenosis; ischemia; diagnosis; peripheral arterial occlusive disease; arterial hypertension. Human soluble guanylylcyclase betal protein AAY51608 standard; Protein; 619 AA. WPI; 2000-184044/17. Schmidt H, Zabel U, (VASO-) VASOPHARM BIOTECH GMBH & 14-AUG-1998; 14-AUG-1998; 24-FEB-2000. DE19837015-A1. Homo sapiens. 26-MAY-2000 (first entry) 98DE-1037015 98DE-1037015 Poller W; 8

N-PSDB; AAZ88939

New human soluble guanylate cyclase alphal/betal and the nucleic acid

developmental biology;

cell signalling;

insecticide;

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NO 1239

(first entry)

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RESULT 2
ABB58149
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AC ABB5
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               ABB58149;
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Pred. No. 5.4e-306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates
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          EINVAAKSQVDAKKDEVPDDMEFL----CEAPLISPATFCKVFPFHLMFDRQMKIVQAGK
                                                                           NNNDGQQIASETDPSIALSTCPIAQDSFDCDGDKEQKCLRLLKNKSDDIERYDHVQFLIR
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The invention relates to an isolated nuclei acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
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The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published_pct_sequences.
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YKIIERGEIDVKGKGTMGTYWLEEREN
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                       FHLEHRGPVSMKGKKEPMQVWFLSRKN
                                                 GVHSGAVVAGIVGLKMPRYCLFGDTVNTASRMESTSIAMKVHISEST-KVLIG---
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AAY70475 standard; Protein; 690 ₽

AAY70475;

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cyclic nucleotide-associated protein-3 (CNAP-3).

AAY70474
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MW GYC
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KW ant: Cyclic nucleotide-associated protein-3; CNAP-3; human; cytostatic; anti-interiosclerotic; hepatotropic; anti-leukaemic; anti-inflammatory; immunomodulatory; anti-asthmatic; anti-anaemic; anti-diabetic; diagnosis; anti-sclerotic; dermatological; neuroprotective; anti-epileptic; cancer; anti-flabetmer's; anti-Parkinsonian; cerebropic protective; ophthalmological; anti-infertility; anti-allergic; vasotropic; immunosuppressive; hypotensive; gene therapy; prevention; treatment; arteriosclerosis;

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identified by PFAM analysis; CNAP-3 shares 89%
identity with human soluble guanylate cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferative disorders (e.g. arterlosclerosis, cirrhosis, leukaemia, lymphoma and cancer of the breast, prostate, lung and brain), autoimmune/inflammatory disorders (e.g. asthma, anaemia, diabetes mellitus, multiple sclerosis and psoriasis), neurological disorders (e.g. epilepsy, Alzheimer's/Parkinson's disease and strokes), vision disorders (e.g. conjunctivitis, glaucoma, cataracts and retinitis pigmentosa), reproductive disorders (e.g. infertility, uterine fibroids, ectopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNAP sequences may be used for prevention, treatment and diagnosis of diseases associated with altered CNAP expression such as, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a human cyclic nucleotide associated protein-3 (CNAP-3), identified in Incyte clone 159278, that is isolated from ADENINBOL CDNA library. It is expressed in nervous, reproductive, cardiovascular and developmental tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
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                                                                       ILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGF
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                                                                                                                                                                                                                                This invention describes novel purified human soluble guanylate cyclase alphal/betal (hsGCalphal/betal). The products of the invention have antiarteriosclerotic, vasotropic and hypotensive activity. Nucleic acid sequences encoding the alphal and/or betal subunit are useful for somati gene therapy of arteriosclerosis and restenosis, ischemia (infarct), peripheral arterial occlusive disease and arterial hypertension.

Antibodies to hsGCalphal/betal can be used for diagnosis of aberrant hsGCalphal/betal expression in human tissues. This sequence represents the human soluble guanylylcyclase alphal subunit described in the method
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                                                                                                                                                                                                                                                                                                                                                                                               New human soluble guanylate cyclase alphal/betal and the nucleic avenceding the subunits, useful for producing diagnostic antibodies, for somatic gene therapy of arteriosclerosis -
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16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
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08-DEC-2000;
08-DEC-2000;
24-JAN-2001;
Detecting a prostate cancer-associated transcript in patient, useful for diagnosing prostate cancer (PC) c modulators of PC, by determining if prostate cancer-a
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DB; ABK92259.
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2000US-0733288.
2000US-0733742.
2001US-263957P.
2001US-276791P.
2001US-276888P.
2001US-286214P.
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RESULT 7
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ABG61800-ABG61944 represent prostate cancer—associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The meticomprises contacting a biological sample from the patient with
ABG61878;
                            ABG61878 standard;
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                                                                                                 ANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPG
                                                                                                                              TSRTETTGEKGKINVSEYTYRCL-----MSPENSDPQFHLEHRG
                                                                                                                                                                                      HHARSICHLALDMMETAGOV-OVDGESVOITIGIHTGEVVTGVIGORMPRYCLEGNTVNL
                                                                                                                                                                                                                                    NAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCI
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                                                                                                                                                            THAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTL
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                            Protein;
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Pred. No. 1.5e-67;
96; Mismatches 219;
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cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-2000;
08-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. ABG61800-ABG61944 represent prostate cancer-associated proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Page 363; 436pp; English.
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30-APR-2001;
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16-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit
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DB; ABK92193.
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                                                                                                                                                                                                                                                                                                 Similarity
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CSEFVNQPYLLYSVHMKSTKPS-----LSPSKPQSSLVIPTSLFCKTFPFHFMFDKD
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2001US-276888P.
2001US-281922P.
2001US-286214P.
2001US-286214P.
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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABS57737-ABB72072).
                                                                                                                  Disclosure; SEQ ID NO 918; 21pp + Sequence Listing; English.
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N-PSDB; ABL02145.
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genes from Drosophila and
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at ftp.wipo.int/pub/published_pct_sequences.
                                                                        WO200171042-A2
                                                                                                               Drosophila melanogaster
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2000US-0614150.
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Pred. No. 2.9e-59;
3; Mismatches 264
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                                                                                   Query Match
Best Local Similarity
Matches 193; Conserv
                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukarytes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                   Sequence
                                                                                                                                                                    The sequence data specification, but
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                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                         genes from Drosophila
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                                                                                                                                                                                           ABB57737-ABB72072
                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                             invention relates to an isolated nucleic acid detection reagent
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                                                          MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
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                                    MYGMLYESVQHYVQEEYGVDIWRKVCHIIDC-KHNSFKTHQIYPDKLMPDIAEALSACTG
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                                                                                                                                                                                                                                                                                                      SEQ ID NO
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                                                                                   Conservative
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2000US-0614150
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                                                                                 Score 685; DB 22;
Pred. No. 2.2e-57;
2; Mismatches 256;
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                                                                                                                                          EP1033401-A2
                                                                                                                                                                                  gene
                                                                                                                                                                                            Human;
                                                                                                                                                                                                              Human secreted protein,
                                                                                                                                                                                                                                   06-OCT-2000
                                                                                                                                                                                                                                                                          AAG00754 standard; Protein; 119
          N-PSDB;
                                      Dumas Milne Edwards
                                                                              26-FEB-1999;
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                                                          (GEST ) GENSET
         2000-500381/45.
DB; AAC00760.
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                                                                                                                                                                                          protein;
                                                                                                                                                                                           cDNA isolation;
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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID 4835; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                              ye number
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Matches 117;
 AAU11280 standard;
                                                                           61
                                                                                        61 LNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIYPGMRAPS
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                                                                                                                                                  1 MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
                                                                                                                                    MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
                                                                          LNAGETLQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIXXGMRAPS
                                                                                                                                                                                                 Conservative
Protein;
 1061
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. No. 3.3e-50;
ismatches 2;
                                                                                                                                                                                                Indels
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                                                                                                                                                                                              Gaps
                                                                                                      119
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Query Match Best Local

Local

Similarity

18.5%;

Score Pred.

Length 119;

Sequence

119

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RESULT 12
AAU11280
                                                                                           Human; natriuretic peptide receptor A/guanylate cyclase A; NPI
atrionatriuretic peptide receptor A; haplotyping; cytostatic;
haplotype pair; single nucleotide polymorphism; gene therapy;
WO200179231-A2
                                   Homo sapiens.
                                                                          haplotype pair;
drug screening;
                                                                                                                                                                              Human
                                                                                                                                                                                                                    12-MAR-2002
                                                                                                                                                                                                                                                         AAU11280
                                                                                                                                                                            atrionatriuretic
                                                                                                                                                                                                                 (first entry)
                                                                          hypertension;
                                                                                                                                                                          peptide
                                                                          hypotensive
                                                                                                                                                                          receptor
                                                                                                                                                                          A (NPR1) protein
                                                                                                                genotyping;
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25-OCT-2001

Genotyping human natriuretic peptide receptor A/guanylate cyclase of an individual, involves determining identity of nucleotide pair specific polymorphic sites for two copies of the gene

pair

gene

Claim

27;

Fig

ω

96pp; English.

N-PSDB;

AAS16995

2002-066340/09.

Bentivegna SC,

Cho1

JY,

Kliem

SE,

Nandabalan

(GENA-) GENAISSANCE PHARM INC

14-APR-2000;

2000US-197330P

16-APR-2001; 2001WO-US12300

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CC (atrionatriuretic peptide receptor A) yearly acte by conserved (atrionatriuretic peptides receptor A) or NPRI polypeptide. A method for CC (atrionatriuretic peptide receptor A) or NPRI polypeptide. A method for CC nucleotide at one or more polymorphic sites and determining whether one CC of the copies of the gene is defined by one of the NPRI haplotypes given in the specification or whether both copies are defined by a haplotype copair. This method is useful in genotypha, whereby all possible haplotype can be assigned to specific genotypes. An association between a CC identified by comparing the frequency of the NPRI gene can be comparing the trait with the frequency of the haplotype pair in a reference population, where a higher haplotype cor haplotype pair the trait with the frequency of the haplotype cor frequency in the trait population indicates the trait is associated with the haplotype or haplotype pair. NPRI and its corresponding DNA are used CC for studying the expression and function of NPRI, for use in screening CC for studying the expression and function of NPRI, set in screening CC or candidate drugs to treat diseases related to NPRI activity, such as CC hypertension. The sequences are also useful for studying the effect of variation on the biological activity of NPRI as well as on the binding CC affinity of candidate drugs targeting NPRI. This sequence represents the Number of NPRI and the sequence represents the Number of NPRI and the sequence represents the Number of NPRI as well as on the binding can be number of NPRI as well as on the binding the Number of NPRI as well as on the binding can be number of NPRI as well as on the binding can be number of NPRI as well as on the binding can be number of NPRI as well as on the binding can be number of NPRI as well as on the binding can be number of NPRI as well as well as on the binding can be number of NPRI as well as well as well as well as well as well as well as well as well as well as well as well as well as well as well as well as well as we
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Best Local
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197; Conserv
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                                                                                                                    MEIAGQVQV---DGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKG
                                                                                                                                                                                                                                    TLLNDLYTCFDAVID----NFDVYKVETIGDAYMVVSGLP---VRNGRLHACEVARMALAL
                                                                                                                                                                                                                                                                                      NLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCIH----HARSICHLALDM
                                                                                                                                                                                                                                                                                                                                                                                                   RKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAEST----PMQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                            KKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRRGLYLSDIPL-----HDATRDL------VLLGEQ--FREEYKLTQELEIL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ntion relates to single nucleotide polymorphisms the human natriuretic peptide receptor A/guanyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CWAEDPQERPPFQQIRLTLRKFNRENSSNILDNLLSRMEQYANNLEELVEERTQAYLEEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EECDHTQFLIEEKESKEEDFYEDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVT
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                                                                          LDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGEAL
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Pred. No. 3.6e-37;
8; Mismatches 227
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NPR1 variant

polypeptide

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RESULT 13
AAU11281
                           cc encoding the human natriuretic peptide receptor Ayguanylate cyclase A (atrionatriuretic peptide receptor Ayguanylate cyclase A (contributed to the peptide receptor Ayguanylate cyclase A (contributed to the peptide receptor Ayguanylate cyclase A (contributed to the peptide receptor Ayguanylate cyclase A (contributed to the peptide receptor Ayguanylate cyclase A (contributed to the peptide receptor Ayguanylate (contributed to the peptide receptor Ayguanylate) (contributed to the peptide receptor Ayguanylate) (contributed to the peptide cyclase) (contributed to the peptide cyclase) (contributed to the peptide cyclase) (contributed to specific genotypes, an association between a cyclastic and a haplotype or haplotype pair of the NRI gene can be cyclastic and a haplotype or haplotype pair of the haplotype on haplotype pair (contributed by comparing the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype for haplotype or haplotype pair. NRI and its corresponding DNA are used cyclastic and the cyclastic and function of NRI, for use in screening cyclastic and the biological activity of NRI as well as on the bidding caffinity of candidate drugs targeting NRI. This sequence represents a human with a collection of the bidding caffinity of candidate drugs targeting NRI. This sequence represents a human with the cyclastic and the cyclastic and the cyclastic and the cyclastic and the cyclastic and the cyclastic cyclastic and the cyclastic and the cyclastic and the cyclastic cyclastic and the cyclastic and the cyclastic and the cyclastic cyclastic and the cyclastic and the cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyclastic cyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of an individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of the gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; atrionatriuretic peptide receptor A; haplotyping; cytostatic; ge haplotype pair; single nucleotide polymorphism; gene therapy; drug screening; hypertension; hypotensive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page -; 96pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bentivegna SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENA-) GENAISSANCE PHARM INC
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341
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                        inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenes;s; proliferation; metastasis; cancer; tumour; hematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; growth haematopolesis regulation; tissue growth; immunomodulator; activin
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      osteoporosis;
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tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
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27-APR-2000; 2000US-0560875
                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                             antifungal; vulnerary; antiulcer.
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Human proteins and DNA encoding sequences useful for preventing treating or ameliorating a medical condition in a mammalian subj .g. arthritis and subject

Claim 20; Page 246-247; 1963pp; English

haematopolesis regulatory activity: tissue growth activity:

immunomodulatory activity: activity: or inhibin-related activities;

chemotactic or chemokinetic activities; haemostatic, thrombotic or

thrombolytic activities; receptor or ligand activities; or may be

involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of

the invention are useful for preventing, treating or ameliorating medical

conditions, e.g., by protein or gene therapy. Such conditions include

cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

proliferative retinopathy, atherosclerosis, coronary heart disease,

arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

vascular growth. Polypeptides involved with tissue regeneration and

repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known protesins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention methave various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides Sequences ABB10981-ABB12330 represent 1350 novel invention. polypeptides, an cell

Sequence 1075

Best Local Matches 1 Query Match al Similarity 197; Conser Conservative 14.98; ,88 Score 481.5; Pred. No. 3. Mismatches .7e-37 В 22; Indels Length 199; 1075; Gaps 31;

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   06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIV 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMRAPSFRCTDAEKGK--GLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRN 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLLNDLYTCFDAVID----NFDVYKVETIGDAYMVVSGLP---VRNGRLHACEVARMALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEL--TRKVLFELKHMRDVQNEHLTRFVGACTDPPNICILTEYCPRGSLQDILENESITL 645
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   9008-0623033
                                                                  90US-0623033
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                                                                                                                                                                                                                                                                                                                                enterotoxin; rat; small intestine;
receptor; bacterial enterotoxin;
ligand; antagonist.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAR38862-63 represent the guanylyl cyclases, GC-A and GC-B, which binds heat stable enterotoxin. These proteins are enterotoxin receptors which may be used as a therapeutic to contintestinal fluid permeation as well as abnormal conditions caused by bacterially released enterotoxin. The binding domain of the proteins, or antibodies to the proteins, can be used to eliminate diarrhoea. The proteins may be used to isolate ligands and to scree for antagonists of toxin binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified enterotoxin receptor protein - used to develop prods. for treating abnormal conditions caused by bacterially released enterotoxin, partic. diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                 VVSGLP---VRNGQLHAREVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVV
                                                                                                                                                                 TVSGLPEPCIH----HARSICHLALDMMEIAGQVQV---DGESVQITIGIHTGEVVTGVI
                                                                                                                                                                                                     TIYFSDIVGFTALSAEST----PMQVVTLLNDLYTCFDAVID----NFDVYKVETIGDAYM
                                                                                                                                                                                                                             TILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYM
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                                                                  GLKMPRYCLFGDTVNTASRMESNGEALKIHLSSETKAVL---EEFD-GFELELRGDVEMK
                                                                                                 GQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLEHRGPVSMK
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                                611
                                                                                                                                                                                                                                                                                                                                           Score 468; DB 14;
Pred. No. 7.2e-36;
8; Mismatches 82;
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420

Search completed: June 27, 2003, Job time: 35.6287 secs 13:03:03

> 1009 593

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM prytein - protein search, using sw model

Run on: June 27, 2003, 13:03:07; Search time 17.4966 Seconds (without alignments) 3401.080 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-762-767A-4
3231
1 MYGFYNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	ر د	4	w	2	ш	Result No.
449.5	450.5	451	453.5	454.5	455.5	456.5	457	466	468	468	470	481.5	646.5	701.5	712	730.5	752.5	770	793	909.5	914	938	955	960.5	987	3188	3206	3231	Score
13.9	13.9	14.0	14.0	14.1	14.1	14.1	14.1	14.4	14.5	14.5	14.5	14.9	20.0	21.7	22.0	22.6	23.3	23.8	24.5	28.1	28.3	29.0	29.6	29.7	30.5	98.7	99.2	100.0	Query Match 1
1025	1047	1525	1047	1047	632	632	1057	1057	1057	1057	1057	1061	947	583	683	717	1099	691	690	732	699	751	686	685	682	619	619	619	Length [
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hypothetical prote	guanylate cyclase	guanylate cyclase	natriuretic peptid	atrial natriuretic	natriuretic peptid	guanylate cyclase	atrial natriuretic	natriuretic peptid	guanylyl cyclase A	atrial natriuretic	hypothetical prote	natriuretic peptid	hypothetical prote	protein C54E4.3 [i	guanylate cyclase	guanylate cyclase	hypothetical prote	guanylate cyclase	guanylate cyclase	guanylate cyclase,				hypothetical prote			guanylate cyclase		Description

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361 EEYKLTQELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNV 420

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415.5 415.5	419 418 416	424 422 420	425	429 428.5	438.5 431.5	443 438.5
12.9 12.9	13.0 12.9 12.9	13.1 13.1 13.0	13.2 13.1	13.3 13.3	13.6 13.4	13.7 13.6
540 1110	1103 1122 1130	1108 1102 1108	1050	1012 1108	1112 1005	1056 1110
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T34187 I59370	JC5581 T28130 A89130	159385 JH0717 B55915	S45636 T42382	T24384 A55915	T28082 S33525	T33167 S55279
hypothetical prote guanylate cyclase	guanylate cyclase hypothetical prote protein F52El.4 [i	guanylate cyclase guanylate cyclase guanylate cyclase	natriuretic-peptid guanylate cyclase	hypothetical prote guanylate cyclase	hypothetical prote guanylate cyclase	hypothetical prote guanylate cyclase

ALIGNMENTS

Db	Qy	Db	ΩУ	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Query Match Best Local : Matches 61	A; Cross-1 A; Cross-1 A; Map pos C; Superfa C; Keyword F; 373-607	A; Residues: A; Cross-ref C; Genetics:	A; Accessi	A;Title:	R;Giuili,	C;Date: 1	guanylate	RESULT 1	
301 ISCLELKGQMIYLPEADSILFICSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEQFR 360	301 ISCLRLKGQMTYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLYLLGEQFR 360	241 PQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTE 300	241 PQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGILDVEKLECEDELTGTE 300	181 IEEKESKEEDFYEDLDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVTQCGNAIYRVL 240	181 IEEKESKEEDFYEDLDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVTQCGNAIYRVL 240	121 RCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFL 180	121 RCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFL 180	61 LNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIYPGMRAPSF 120	61 LNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIYPGMRAPSF 120	1 MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN 60	1 MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN 60	<pre>/ Match 100.0%; Score 3231; DB 1; Length 619; Local Similarity 100.0%; Pred. No. 1.1e-215; nes 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	A;Cerue: our socials; occass; occass, across-references; GDB:141992; OMIM:139397 A;Map position: 4q31.3-4q33 C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology C;Reywords: heterodiner; phosphorus-oxygen lyase F;373-607/Domain: guanylate cyclase catalytic domain homology <gcc></gcc>	A;Residues: 1-619 <giu> A;Cross-references: EMBL:X66533; NID:g31685; PIDN:CAA47144.1; PID:g31686 C;Genetics:</giu>	A; Accession: S23097 A; Accession: Lippe: mRNA A; Molecule type: mRNA	A; Title: Molecular cloning of the cDNAs coding for the two subunits of soluble guanyl A; Title: Molecular cloning of the cDNAs coding for the two subunits of soluble guanyl A; Reference number: S23007; MOTD: 92316204: PMTD: 1352257	C;ACCESSIUN: 52307; R;Giuili, G.; Scholl, U.; Bulle, F.; Guellaen, G. FFRG Lett 304 93-89 1003	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000	guanylate cyclase (EC 4.6.1.2), soluble, 70K chain - human		

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RESULT 2

OYBO70

OYBO70

OYBO70

Guanylate cyclase (EC 4.6.1.2), soluble, beta-1 chain - bovine guanylate cyclase, soluble, 70K chain C; Species: Bos primigenius taurus (cattle) C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change C; Accession: S01653; A8759

R; Koesling, D.; Herz, J.; Gausepohl, H.; Niroomand, F.; Hinsch, FEBS Lett. 239, 29-34, 1988

A;Title: The primary structure of the 70 kDa subunit of bovine A; Reference number: S01653; MUID:89031214; PMID:2903071

A; Accession: S01653

A; Molecule type: mRNA

A; Residues: 1-619 <KOE>

A; Cross-references: EMBL:Y00770; NID:g407; PIDN:CAA68739.1; PII A; Accession: A38759

A; Molecule type: protein

A; Residues: 1-6; 28-32;41-45;96-109;337-343;396-406;562-569 <KOI C; Genetics:

A; Introns. 781/3. 302/2
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C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic
C;Keywords: cGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
F;373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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Pred. No. 5.8e-214;
5; Mismatches 1;
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A; Title: Molecular cloning of a cDNA coding for 70 kilodalton A; Reference number: A31871; MUID:89087429; PMID:2905128
A; Molecular the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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A; Molecule type: mRNA
A; Residues: 1-619 <NAK>
A; Residues: 1-619 <NAK>
A; Cross-references: GB:M22562; NID:g204273; PIDN:AAA41204.1; PID:g204274
C; Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic dor
C; Keywords: cGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
E; 373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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guanylate cyclase (EC 4.6.1.2), soluble, beta-1 chain - rat
N;Alternate names: guanylate cyclase, soluble, 70K chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A31871
C;Accession: A31871
R;Nakane, M.; Saheki, S.; Kuno, T.; Ishii, K.; Murad, F.
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Pred. No. 1e-212;
5; Mismatches 4;
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R;Yuen, P.S.T.; Potter, L.R.; Garbers, D.L. Blochemistry 29, 10872-10878, 1990
A;Title: A new form of guanylyl cyclase is A;Reference number: A36228; MOID:91105012; A;Accession: A36228
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OYRTB2

guanylate cyclase (EC~4:6.1.2), soluble, beta-2 chain - rat

guanylate cyclase; soluble, 76K chain

N;Alternate names: guanylate cyclase, soluble, 76K chain

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
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A; Residues: 1-682 < YUE>
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R; Yuen, P.S.T.; Pot
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Pred. No. 2.4e-60;
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A; Accession: T23092
A; Status: preliminary; t:
A; Molecule type: DNA
A; Residues: 1-685 <WI2>
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A; Accession: T19968
A; Status: preliminary
A; Molecule type: DNA
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A; Introns: 11/3;
C; Superfamily: so
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KKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGFN---AFCSKHASGEGAM
                              TSIPELLOYGLRLTAMPIHDPTRDLILLNQQRLSDVEMNLQLEANNEQLENMAKDLEVEK
                                                                                              MEFQRNANKRAAQAIEASENLYEDNNGALALSQSQHLKLKGQMMLMSSGGHIMYLCSPYV
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oluble guanylate cyclase; guanylate cyclase
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ce: clone C46E1
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RESULT 6 RESULT 6 REPROLICATION PROTECTION	
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C;Speckes: Caenorhabditts elegans
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C;Accession: T18984
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A; Map position: 5
A; Introns: 1/3; 60/1; 192/3;
C; Superfamily: soluble guanyl
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A; Residues: 1-699 <WIL>
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-CSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPFVYKVETVGDKYMTVS
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32.9%; Pred. No. 2.8e-55;
Live 132; Mismatches 234;
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(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
(;Accession: S18325
R;Harteneck, C.; Wedel, B.; Koesling, D.; Malkewitz, J.; Boehme, E.; Schult:
FBBS Lett. 292, 217-222, 1991
A;Title: Molecular cloning and expression of a new alpha-subunit of soluble
A;Reference number: S18325; MUID:92070494; PMID:1683630
A;Accession: S18325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-732 <HARN
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                                                                                                                                LNDLYTRFDTLTDSRKNPF--VYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIA
                                                                                                                                                                                       TVDLLYSIFPGDVAQQLWQGQQVQARKFDDVTMLFSDIVGFTAICAQCT----PMQVISM
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1; Mismatches 175;
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homology

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guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - rat
N.Alternate names: guanylate cyclase, soluble, 77K chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A38297
C;Accession: A38297
C;Rakane, M.; Arai, K.; Saheki, S.; Kuno, T.; Buechler, W.; Murad, F.
J. Biol. Chem. 265, 16841-16845, 1990
A;Title: Molecular cloning and expression of cDNAs coding for soluble guanylate cyclase
A;Reference number: A38297; MUID:91009100; PMID:1698769
A;Accession: A38297
A;Molecula type: mRNA
A;Residues: 1-690 <NAK>
A;Cross-references: GB:M57405; GB:M36075; NID:9204277; PIDN:AAA41206.1; PID:9204278
C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C;Keywords: GGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
F;432-660/Domain: guanylate cyclase catalytic domain homology <GCC>
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                                                 RGPVSMKGKKEPMQVWF
                                                                                                                 LTSRTETTGEKGKINVSEYTYRCL---
                                                                                                                                                   DTHAVQIALMALKMMELSNEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVT
                                                                                                                                                                                 IHHARSICHLALDMMEIAGQV-QVDGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVN
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                                                                                                                 ------MSPENSDPQF-----HL----EH
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A; Residues: 1-691 < KOE1>
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Local Similarity
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                                                                                SDPQF 582
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C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic C;Keywords: cGMP blosynthesis; heterodimer; phosphorus-oxygen lyase F;434-662/Domain: guanylate cyclase catalytic domain homology <GCC>
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A;Title: The primary structure of the larger subunit of A; Reference number: S10713; MUID:90306336; PMID:1973124
A; Accession: S10713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 118-133,226-232;286-293;319-330;412-417;557-571;629-637 < XOE 2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X54014; NID:g405; PIDN:CAA37960.1; PID:g406
A;Accession: A38767
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                                                                                                                                                                        VYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQ-VQVDGESVQITIGIHTGE
                                                                                                                                                                                                                                                                    KRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPF
                                                                                                                                                                                                                                                                                                                                                                                                                 TRDLVLLGEOFREEYKLTOELETLTDRLQLTLRALEDEKKKTDTLLYSYLPPSVANELRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLECEDELTGTEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQCGNAIYRYLPQLQ-PGNCSLLSVFSLVRPHIDISFHGILSHINTVFYLRSKEGLLDVE
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   VFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREE
                                                       VVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCL------MSPEN
                                                                                                                 VYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMELSHEVVSPHGEPIKMRIGLHSGS
                                                                                                                                                                                                                                     GHAVQAKREGNVTMLESDIVGETAICSQCS----PLQVITMLNALYTREDRQCGELD---
                                                                                                                                                                                                                                                                                                                                                          LRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKRKTVDLLCSIFPSEVARQLWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQLGHGIRRLMSRRDVQGKPHFDEYFEILTPKISQTFSGIMTMLNMQFLVRVRRW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -FHQDCREFVDQPCELYSVHIRSARPHPPPGKPVSSLVIPASLFCKTFPFHFMLDRDMSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFLIEEKESKEE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGVVGGTLKDFLNSFSTL------LKQSSHCQEAEK-KGRFEDASILCLDKDPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILRVLGSNVREFLQNLDALHDHLATIYPGMRAPSFRCTDAEKGKG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DNSMKKSSRVMDLKGQMIYMVESSSILFLGSPCVDRLEDFTGRGLYLSDIPIHNA
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Pred. No. 2.5e-45;
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hypothetical protein T07D1.1 - Caenorhabditis elections, Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Accession: T16822
R;Leimbac, D.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the sequence of C. elegans cosmid of the cosmid of the sequence of C
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A:Tntrons: 26/3; 94/3;
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A; Reference number: Z18584
A; Accession: T16822
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211; Conservative
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                                                                                                                           QFERREEIEIK-DDQTIQTEFVVSRHGPHRVPSPRNC---ESRQDD
                                                                                                                                                                          HLEHRGPVSMKGKKEPMQVWFL-----SRKNTGTEETKQDD 618
                                                                                                                                                                                                                                                                                                                                --VYKVETIGDAYMVVSGAPTKTEHDAEFILDCASQFLVEAGKMVNMNNKIHKIDIRAGV
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                                                                                                                                                                                                                                                                              HTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGERGKINVSEYTYRCLMSPENSDP-QF
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4.6.1.2),
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guanylate cyclase (EC 4.6.1.2) - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C;Date: 03-Feb-1994 *sequence_revision 03-Feb-1994 *text_change 26-Aug-1999
C;Accession: JH0810
R;Yoshikawa, S.; Miyamoto, I.; Aruga, J.; Furuichi, T.; Okano, H.; Mikoshiba, K.
J. Neurochem. 60, 1570-1573, 193
A;Title: Isolation of a Drosophila gene encoding a head-specific guanylyl cyclas
A;Reference number: JH0810; MUID:93203896; PMID:8095978
A;Recession: JH0810
A;Molecule type: mRNA
A;Residues: 1-683 <YOS>
A;Cross-references: GB:S57126; NID:9298674; PID:g298675
A;Experimental source: head
C;Genetics:
A;Gene: dgc 1
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A; Accession: $23098
A; Molecule type: mRNA
A; Residues: 1-717 <GIU>
A; Cross-references: EMBL:X66534; NID:g31683; PIDN:CAA47145.1;
C; Superfamily: soluble guanylate cyclase; guanylate cyclase ca
C; Keywords: heterodimer; phosphorus-oxygen lyase
F;430-658/Domain: guanylate cyclase catalytic domain homology
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S23098
R;Giuili, G.; Scholl, U.; Bulle, F.; Guellaen, G.
FEBS Lett 304, 83-88, 1992
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domain homology

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protein C54E4.3 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C; Accession: F88642
R; Anonymous, The C; elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A; Title: Genome sequence with period of the nematode C. elegans: a platform for investigating biolog
A; Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A; Accession: F88642
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-583 <STO>
A; Cross-references: GB:chr_IV; PIDN:AAB92031.1; PID:g2702405; GSPDB:GN00022; CESP:C54E4.
A; Note: Similar to guanylate cyclase
C; Genetics:
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C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic
C;Keywords: cGMP biosynthesis; phosphorus-oxygen lyase
F;417-641/Domain: guanylate cyclase catalytic domain homology <GCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVTILESDIVGFTSICSRAT----PFMVISMLEGLYKDFDEFCD----FFDVYKVETIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGIIERAFRCLGTDLQEFLGSLDGVYDVLKLQEEDVTDTGFVCA----GEGELI-FTS
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No. 2.6e-41;
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A; Gene: C54E4.3
A; Map position: 4
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Best Local
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LENKKTLKVSDLMQLVQPSDIQLTYKNVLSYLNTLFIFQLKH----HSKRNEVQEGSSEAF
                                      QLQPGNCSLLSVFSLVRP-HIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTE
                                                                                                                    EDILDREEENGTQESRISPYT------FCKAFPFHIIFDRDLVVTQCGNAIYRVLP
                                                                                                                                                            FPIVKGLVRKTARTLF--EMDVKVCMLERNQERRKSGMVEHVIFSVEPDDNHRKGKRLFH
                                                                                                                                                                                                    QDIVIGIIKTVAQQIHGTEIDMKV-IQQRNEE-----CDHTQFLIEEKESKEED---FY
                                                                                                                                                                                                                                             MLFCMANNLQEFLDNLNSMHYFIDQIA-FKSEMKGPTFQCEPFGE-SGLKLHYFSFRQGL
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                                                                                                                                                                                                                                                                                                                           RRKAGYQEDIKFDIQCYYDDTETMRIFRVAATVLGLSVDDMWEMYGEFLITHACETGWQK
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                -KFRNTKTTENAPS-FTLSSTILVGLRDFKNIFPYHVCFNKQMIIEHIGIYLLREYG
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Pred. No. 1.1e-40;
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CGPVVAGIVSQQKPRFCVLGNTVNVTKSICSHSSPGKVLVS 578 TGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVS ---YKVLSLMDSYLIVGGVPNANQYHCEDSLNLALGLLFEAKQVVVPKLERSVRLRIGVH PFVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQVQVD--GESVQITIGIH SIDFSEEFSDCSVIFTDIPDFFTISVNCS-----PTEIITVVTDLFHRFDRIIEKHKG ----KRYDNVTILFSGIVGF---NAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKN

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CQMELNKKLEETMKKMKKMTEELEVKKSQTDRLLFEFVPPVIAEALRAAKTVPALMQKRI

EEYKLTQELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPA-----QQPLVLKGEMMPINDGNSIIFICSPHVTTVRDILNLKLYISDMPMHDATRDLVMLNQSRI

414 367

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300 250 241

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

June 27, 2003, 12:55:07 ; Search time 11.0695 Seconds (without alignments) 2585.358 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-762-767A-2 3593 1 MFCTKLKDLKITGECPFSLL.....QKKDVEDGNANFLGKASGID 690

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25 438 12.1 1103 26 434 12.1 1103 27 430 12.0 1110 28 428.5 11.9 1050 29 427 11.9 1125	434 12.1 434 12.1 430 12.0 428.5 11.9	438 12.2 434 12.1 430 12.0	436 12.2		438 12.2	440 12.2	442 12.3	445 12.4	448 12.5	450 12.5	452 12.6	454.5 12.6	456.5 12.	460 12.8	460 12.8	460 12.8	708 19.7	774.5 21.6	789.5 22.0	793.5 22.1	795 22.1	976.5 27.2	1635 45.5	46.0	86	90.0	1 3593 100.0 69	Result Query No. Score Match Length
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ALIGNMENTS

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	SWISS-PROT entry is copyright. It is produced through a coen the Swiss Institute of Bioinformatics and the EMBL ouropean Bioinformatics Institute. There are no restricting non-profit institutions as long as its content is led and this statement is not removed. Usage by and for ies requires a license agreement (See http://www.isb-sib.cnd an email to license@isb-sib.ch).	77(1998). WITY: GTP = 3',5'-cyclic GMP + diphosphate. ION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF ANGANESE IONS. DIMER OF AN ALPHA AND A BETA CHAIN. DATION: Cytoplasmic. THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE RANE-ASSOCIATED RECEPTOR FORMS. LONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE	TISSUE-KIGNEY, Gansemans Y., Brouckaert P., Fiers W.; "Human soluble guanylate cyclase large subunit mRNA, alpha3-like."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. [3] SEQUENCE FROM N.A. TISSUE-Brain; MEDLINE-98416113; PubMed-9742212; Tabel U., Weeger M., La M., Schmidt H.H.; "Human soluble guanylate cyclase: functional expression and revised isoenzyme family.";	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUB-Brain; MEDLINE-92316204; PubMed-1352257; MEDLINE-92316204; PubMed-1352257; Giuili G., Scholl U., Bulle F., Guellaeen G.; Giuili G., Scholl U., Bulle F., Guellaeen G.; Molecular cloning of the cDNAs coding for the two subunits of "Molecular cloning of the cDNAs coding for the two subunits of "Boluble guanyly1 cyclase from human brain."; FEBS Lett. 304:83-88(1992).	CYG3_HUMAN STANDARD; PRT; 690 AA. CYG3_HUMAN STANDARD; PRT; 690 AA. Q02108; O43843; 01-JUL-1993 (Rel. 26, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1) (Soluble guanylate cyclase large subunit) (GCS-alpha-3). GUCY1A1 OR GUCY1A3 OR GUCIA3 OR GUCSA3. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MCBI_TaxID-9606;	LT 1

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Query Match
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CONFLICT
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MIM; 139396; -.
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                                           VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
                                                                                                                                  TMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHK
                                                                                                                                                                                                           FGNGIRRLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKKS
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                                                                                                                                                                                                                                                                                                                                                                                                                               MFCTKLKDLKITGECPFSLLAPGQVPNESSEEAAGSSESCKATVPICQDIPEKNIQESLP
                                                                                                                       TMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHK
                                                                                                                                                                                                                         SRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQAR
                                                                                                                                                                                                                                                                                                                                                                                     QAVAAGVPVEVIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFSTLLKQSSHCQEAG
                                 VTLANKFESCSVPRKINVSPTTYRLLKDCPGEVETPRSREELPPNFPSEIPGICHFLDAY
                                                                                                                                                                 AQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNV
                                                                                                                                                                           AQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNV
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GDAYCVA -> AMPIVWL (IN REF. 1).

GNANFLGKASGID -> ASQFFRQSIRNRLATYIPIYKSLG

FDSLKWCRASESTLGIVDG (IN REF. 1).

DA1E14A5E11451CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUANYLATE CYCLASE.
AAGV -> QQS (IN REF. 1).
VIRESJGEFWRKICYEBDENIJGVVGGTLKDFLNSFSTLLK
QSSHCQEAGKRGR -> LSKNLLVKRFLKYVTRKMKTSLGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 3593; DB 1;
Pred. No. 2.7e-243;
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                                                                                                           SEQUENCE
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                                                                            Local
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61
QRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESRKSLEREDFEKTIAE
                     MFCRKFKDLKITGECPFSLLAPGQVPTEPIEEVAGVSESCQATLPTCQEFAE-NAEGSHP
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661
QQGTNSKPCFQKKDVEDGNANFLGKASGID 690
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prenatally in the rat brain.";

Brain Res. Dev. Brain Res. 97.226-234(1996).

-I CATALYTIC ACTIVITY: GTP = 3',5'.cyclic GMP + diphosphate.
-I ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESEN
MAGNESIUM OR MANGANESE IONS.
-I SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-I SUBCELLULAR LOCATION: Cytoplasmic.
-I MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
-I SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC
(Soluble guanylate cyclase large subunit).
                                                                                                                                                                                                                                                                          Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCc; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

Lyase; CGMP synthesis; Multigene family.

Lyase; CGMP Synthesis; Multigene family.

GUANYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and expression of cDNAs guanylate cyclase from rat lung.";
J. Biol. Chem. 265:16841-16845(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley;
MEDLINE-97151525; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M57405; AAA41206.1;
EMBL; U60835; AAB17953.1;
PIR; A38297; OYRTA1.
HSSP; P19687; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smigrodzki R.M., Levitt P.; "The alpha 1 subunit of soluble guanylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUCY1A1 OR GUC1A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE-91009100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro; IPR001054; G_cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EL European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                      al Similarity
616; Conserv
MFCTKLKDLKITGECPFSLLAPGQVPNESSEEAAGSSESCKATVPICQDIPEKNIQESLP
                                                                                                                                                                                                                                                690 AA;
                                                                                                      Conservative
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                                                                                                  Score 3232; D
Pred. No. 4.3e
99; Mismatches
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                                                                                                                                   .3e-218;
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FEBS Lett. 266:128-132(
[2].
3D-STRUCTURE MODELING O
MEDLINE-98054247; PubMe
Liu Y., Ruoho A.E., Rao
                                                                               cyclase f
                                                                                                                    Koesling
Schultz G
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC
(Soluble guanylate cyclase large subunit).
GUCYIA1 OR GUCIA1.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Verte
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                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL S TISSUE-Adrenal medulla; MEDLINE-90306336; PubMed-1973124;
                                                                                                                                                                                                        Mammalia; Eutheria;
Bovidae; Bovinae; Bu
NCBI_TaxID=9913;
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P19687;
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G., Boehme
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EAIAAGVPVEVLKDSLGEELFKICYEEDEHILGVVGGTLKDFLNSFSTLLKQSSHCQEAE
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                                                           266:128-132(1990)
                                                                                       structure of bovine lung.
                                                                                                                                  Harteneck C., Humbert P.,
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
 ELING OF 472-628.
; PubMed=9391039;
E., Rao V.D., Hurl
                                                                                                                                                                                                                           Bos.
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    Hurley
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RT "Catalytic mechanism of the adenylyl and guanylyl cyclases: modeling RT and mutational analysis.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).

CC -: CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

CC -: ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF MAGNESIUM OR MANGAMESE IONS.

CC -: SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

CC -: SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

CC -: MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

CC -: SIMILARITY: BELONGS TO ADENVLYL CYCLASE CLASS-4/GUANYLYL CYCLASE

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstatton - CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cor send an email to license@isb-sib.ch).
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EMBL; X54014; CAA37960.1; -.

PIR; S10713; OYBO77.

PIB; 1AWN; 28-JAN-98.
InterPro; IPR001054; G_Cyclase.
Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

SMART; SM00045; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.

Lyase; CGMP synthesis; Multigene family; 3D-structure.
DOMAIN 482 609 GUANYLATE CYCLASE.

SEQUENCE 691 AA; 77532 MW; 5DIFE4D2204E8683 CRC64;

SEQUENCE 691 AA; 77532 MW; 5DIFE4D2204E8683 CRC64;

Query Match

86.5%; Score 3107.5; DB 1; Length 691;

Best Local Similarity 86.1%; Pred. No. 2.1e-209;

Matches 595; Conservative 41; Mismatches 54; Indels 1; Gaps 1;

MECTRIKDLKITGECPFSILAPGQVPNESSEEAAGSSESCKATVP-ICQDIPEKNIQESL 59

1 MECAKLKDLOITGDCPFSILAPGQVPREPLGEATGSGPASTEGOPGVCPGVPDKNPPGRI. 60

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Matches 355;
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Pfam; PP60211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

SMO044; CYCC; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.

Lyase; CGMP synthesis; Multigene family.

DOMAIN 519 646 GUANYLATE CYCLASE.

DOMAIN 50 72 ALA-RICH.

DOMAIN 50 72 POLY-ALA.

SEQUENCE 730 AA; 81786 MW; B8D790BFF81FB8F9 CI
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STRAIN-Wistar Kyoto; TISSUE-Aorta;
MEDLINE-20571097; PubMed-11121588;
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an email to license@isb-sib.ch).
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Harteneck C., Wedel
Schultz G.:
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-2 chain (EC GUCYIA2 OR GUCIA2 OR GUCSA2.
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Mammalia; Eutheria;
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Interchangeability
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PROSITE; PSS0125; GUANYLATE_CYCLASES_2; 1.

LYABE; cGMP synthesis; Multigene family; Alternative splicing.

DOMAIN 521 648 GUANYLATE CYCLASE.

DOMAIN 51 76 ALA-RICH.

DOMAIN 51 76 ALA-RICH.

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PARSPLIC 612 612
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EMBL; Z50053; CAA90393.1; -.
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

SUBCELLULAR LOCATION: CYtoplasmic.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-2 (SHOWN HERE) AND ALPHA-2-I; ARE PRODUCTSD BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ALPHA-2 ISOFORM IS EXPRESSED IN FETAL ILIVER, COLON, ENDOTHELIUM AND TESTIS, WHILE THE ALPHA-2-I IS EXPRESSED ONLY IN LIVER, COLON AND ENDOTHELIUM.

MISCELLANDOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
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                                                                                                                                                                                                               GFDALLE---HIRTSFGKQATLESPSFLCKELPEGTLMLHYFHPHHIVGFAMLGMIKAAG
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Q -> QPORSELLESEPVSIQLVPDQHQSETDLGTEK
O TOPORM ALPHA 2-1).
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Pred. No. 1
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Q07093;
01-FEB-1995
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its many modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                   J. Neurochem. 60:1570-1573(1993).

1. FUNCTION: MAY HAVE A ROLE IN PHOTOTRANSDUCTION. A SECOND MAY BE REQUIRED FOR ENDYME ACTIVITY.

1. CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

1. SUBUNIT: DIMER (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Head-specific guanylate cyclase (EC 4.6.1.2).
GYC-ALPHA-99B OR GYC-ALPHA-63A OR GYC OR DGC1.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Canton-S; TISSUE-Head;
MEDLINE-93203896; PubMed-8095978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshikawa S., Miyamoto I., Aruga J.,
Mikoshiba K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolation of a Drosophila gene
                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: HEAD,
THE CNS AND THE RETINA. NO
SIMILARITY: BELONGS TO ADD
                                                                                                                                                                                                                                              SUBCELULAR LOCATION: Cytoplasmic (Potential),
TISSUE SPECIFICITY: HEAD, WHERE IT IS PREFERENTIALLY EXPRESSED IN
THE CNS AND THE RETINA. NOT FOUND IN BODIES.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                             FAMILY.
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Best Local Similarity
Matches 244; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0013972; Gyc-alpha-99B.
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
SMART; SM000452; GUANYLATE_CYCLASES_1; FAI
PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.
Lyase; cGMP synthesis; Multigene family; V1
DOMAIN
465
591
GUANYLATE CYCI
SEQUENCE 683 AA; 75906 MW; 12D67C4B79A0
CYG1_RAT STANDARD; PRT; 619 AA. P20595; P20595; Created) 01-FEB-1991 (Rel: 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Guanylate cyclase soluble, beta-1 chain (EC 4 (Soluble guanylate cyclase small subunit). GUCY1B1 OR GUCY1B3 OR GUCLB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR;
HSSP;
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                                                                                                                                                                               ALKINVSPITKDWLTKHEGFEFELQPRDPSFLPKEFPN--PGGTETCYFLESFR
                                                                                                                                                                                                                                                                   ALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
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Pred. No. 1.3
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Best Local Similarity
Matches 210; Conserv
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SEQUENCE FROM N.A.

MEDLINE-89087429; PubMed=2905128;

Nakane M., Saheki S., Kuno T., Ishii K., Murad F.;

Nakane M., Saheki S., Kuno T., Ishii K., Murad F.;

Molecular cloning of a cDNA coding for 70 kilodalton subunit soluble guanylate cyclase from rat lung ";

Biochem. Biophys. Res Commun. 157:1139-1147(1988).

-I- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

-I- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESEN MAGNESIUM OR MANGANESE IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P16068; 1AWN.
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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PROSITE; PS50125; GUANYLATE_CYCLASES.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: LUNG AND BRAIN.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETERODIMER OF AN ALPHA AND
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DATROLVLLGEQFREEYKLTQELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANEL
                                               NALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQL
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                                                                                                    VEKLECEDELTGAEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                    FRCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRSEECDHTQ-
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                                                                                                                                   SSRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIH
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Sciurognathi; Muridae; Murinae; Rat
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                       The primary structure of t. guanylate cyclase."; FEBS Lett. 239.30
                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-1 chain (EC 4
(Soluble guanylate cyclase small subunit).
GUCY1B1 OR GUCY1B3 OR GUCYB3.
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P16068;
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Muelsch A., Boehme E., Schultz G.,
"The primary structure of the 70 kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
MEDLINE=89031214;
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                           PDB;
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                                                                                                                                                                                                                                                                                                                                    MEDLINE-98054247; PubMed-9391039;
Liu Y., Ruoho A.E., Rao V.D., Hur
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                                                                                                                                                                                                                                                                                                                                                             3D-STRUCTURE MODELING OF 412-572.
                                                                                                                                                                                  SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: CYCOPLASMIC.
TISSUE SPECIFICITY: LUNG AND BRAIN.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL
                                                                                                                     s SWISS-PROT entry is copyright. It is produced th ween the Swiss Institute of Bioinformatics and t European Bioinformatics Institute. There are no
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           1AWN; 28-JAN-98.
                                     S01653;
                                               Y00770; CAA68739.1;
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guanylate_cyc;
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Best Local S
Matches 208
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PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
Lyase; CGMP Synthesis; 3D-structure.

Lyase; CGMP Synthesis; 3D-structure.

DOMAIN 421 554 GUANYLATE (
                                                                                                                                         CYG1_HUMAN STANDARD; PRT; 619 AA. (202153; 201-3UL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (Soluble guanylate cyclase small subunit) (GCS-beta-5 GUCY1B1 OR GUCY1B3 OR GUCYB3 OR GUCSB3.
                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                               GUCYIBI ON THOMO Sapiens (Human).
Homo sapiens (Human).
Motazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                          NCBI_TaxID-9606;
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MEDLINE-92316204; PubMed-1352257; Giuili G., Scholl U., Bulle F., Guellaeen G. "Molecular cloning of the cDNAs coding for t soluble guanylyl cyclase from human brain.";

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PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
Lyase; cGMP synthesis; Alternative splicing
DOMAIN 421 554 GUANYLATE CYCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession
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HSSP; P16068; 1AWN.
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MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ro; IPR001054; G_cyclase. PF00211; guanylate_cyc; 1. SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:4687; GUCY1B3.
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                                                                                                                                                                                                                                DIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQ
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35.1%;
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Pred. No. 1.
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; 231E4E660DE02AA1 CRC64;
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01-AUG-1991
16-OCT-2001
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         InterPro; IPR001054; G_cyclase.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR0011230; Prenyl_site.
IPfam; PF00211; guanylate_cyc; 1.
SMARR; SM00044; CYCC; 1.
SMARR; SM000452; GGANYLATE_CYCLASES_1;
PROSITE; PS00452; GUANYLATE_CYCLASES_2;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                      entities
or send a
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 29:10872-10878(1990).
-!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic
-!- ENZYME REGULATION: ACTIVATED BY NITRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91105/12; PubMed-1980215; Yuen P.S.T., Potter L.R., Garbers D.L.; *A new form of guanylyl cyclase is preferentially expressed kidney.*;
                                                                                                      EMBL; M57507; AAA4120
PIR; A36228; OYRTB2.
HSSP; P19687; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guanylate cyclase GUCY1B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLI FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: KIDNEY AND LIVER.
                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETERODIMER OF AN ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                           MAGNESIUM OR MANGANESE IONS
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                                                                                                                                                                       an
                                                                                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/
nn email to license@isb-sib.ch).
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(Rel. 19, Last sequence update)
(Rel. 40, Last annotation update)
yclase soluble, beta-2 chain (EC 4.6.1.2)
synthesis
                                                                                                                                       AAA41207.1;
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15-JUL-1999 (Rel.:
16-OCT-2001 (Rel.:
16-OCT-2001 (Rel.:
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SEQUENCE
 SEQUENCE OF 95-257
TISSUE-Heart;
MEDLINE-99107820;
                                                        Behrends S., Vehse K.;
Behrends S., Vehse K.;
"The beta(2) subunit of soluble guanylyl cyclase contains human-specific frameshift and is expressed in gastric carronness atomber Res. Commun. 271:64-69(2000).
                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                    GUCY1B2
                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                    Guanylate cyclase
                                                                                                                                            MEDLINE=20241821; PubMed=10777682;
                                                                                                                                                               FISSUE=Kidney;
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40, Last annotation updat
soluble, beta-2 chain (EC
   PubMed-9889008
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AICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIAL
                                                                                       LKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFT
                                                                                                                                                                                                          QTQ-NIQLDEYFSIIHPQVTFNIFSIRRFINSQFVLKTRREMMPVAWQSRTTLKLQGQMI
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                                                                                                                                                                                                                                                                                                                                                                                                                       FLH--YYSDRSGLCHIVPGIIEAVAKDFFDIDVIMDIL-----DMNEEVERTGKKEHVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMPPCFHNDCSEFVNQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRMLRTLGGNLMEFIENLDALHSYLALSYQEMNAPSFRVERGADGKM.
                                                                     KKEELQVLSKHLAIEKKKTETLLYAMLPKHVANQLREGKKVAAGEFKSCTILFSDVVTFT
                                                                                                                                         WMESMWCMVYLCSPKLRSLQELEELNMHLSDIAPNDTTRDLILLNQQRLAEIELSNQLER
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19.7%;

Pred. Score

DB

Length

617;

100;

Mismatches ء 708; ام. 6.

191;

Indels

102;

Gaps

12;

198

51

-SLSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTILQFGNGIRRLMNRR

163

264

251

461

491 341 431 281 371 222 312

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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: G
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and D13S155.";
                                                                                                                                                                                  EMBL; AF038499; AAD09440.2;
EMBL; AF218383; AAF66105.1;
HSSP; P19687; 1AWN.
                                                                                          Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 1.
                                                   PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                             InterPro; IPR001054; G_cyclase.
                                                                                                                                                    Genew; HGNC:4686; GUCY1B2.
MIM; 603695; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assignment of GUCY1B2,
                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLGUAR LOCATION: CYCOPLASMIC.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: GTP = 3',5'-GYGLIC ENZYME REGULATION: ACTIVATED BY NITRIC MAGNESIUM OR MANGANESE IONS.
                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
   617 AA;
                                      synthesis.
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   70367 MW;
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GUANYLATE CYCLASE.
; 186C965CAB9A5E3E CRC64;
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01-NOV-1995
16-OCT-2001
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_BOVIN
                                                                            EMBL;
EMBL;
HSSP;
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"Detection of expression of a membrane form of
type of GC-B in cattle retina (letter).";
Bioorg. Khim. 19:682-685(1993).
-I- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC
   InterPro;
InterPro;
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration hatwaen the Swiss Institute of Bioinformatics and the EMBL outstation hatwaen the Swiss Institute of Figure 1.
                                                                                                                                                                                     modified
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Fenrick R., Babinski K., McNicoll N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOY-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide
                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93371497; PubMed=8103329;
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NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-type receptor).
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                                                         InterPro;
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CATALTYTC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphat SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECE WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND O WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDICTION.

SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CANDOMAIN OF PROTEIN KINASES.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLY
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                                                                    L26359; AAC41619.1;
X66865; CAA47334.1;
Q02846; IAWL.
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                                                                                                                                               non-profit institutions as long
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requires a license agreement (See
an email to license@isb-sib.ch).
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                   IPR001828;
IPR000719;
IPR001054;
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; ANF_receptor.
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Pfam; PF00069; pkinase; 1.

Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF01094; ANF_receptor; 1.

PRINTS; PR00255; NATPEPTIDER.

PRODOm; PD000001; Euk_pkinase; 1.

SMART; SM00044; CYCc; 1.

PROSITE; PS00450; ANF_RECEPTORS; 1.

R PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50115; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                     ANPB_HMAN STANDARD,
ANPB_HMAN STANDARD,
P20594; Q9UQ50; O60871;
P10594;  Q9UQ50; O60871;
P10594; Q9UQ5
                                                                                      NPR2 OR ANPRB.
Homo sapiens (Human)
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Eukaryota; Metazoa; Mammalia; Eutheria;
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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    Phosphorylation;

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Hirsch J.R., Herter P., Wel
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proximal tubule cells.";
Submitted (APR-1998) to the
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"Structure of the type B human natriuretic peptide receptor gene association of a novel microsatellite polymorphism with essential hypertension.";
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TISSUE=Brai
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Genew; HGNC:7944; NPR2.
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SMART; SM00044; CYCC; 1.

PROSITE; PS00458; ANF_ECCEPTORS; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1;

PROSITE; PS50125; GUANYLATE_CYCLASES_2;

PROSITE; PS50111; PROTEIN_KINASE_DOM; 1.
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RESULT 14
ANPB_RAT
                                                                                                                                     Pfam; PF00069; pkinase; 1.

Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF01094; ANF_receptor; 1.

PRINTS; PR000255; NATPEPTIDER.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00044; CYCG; 1.

PROSITE; PS00458; ANF_RECEPTORS; 1.

PROSITE; PS00458; ANF_RECEPTORS; 1.

PROSITE; PS00458; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS5011; PROTEIN, KINASE_DOM; 1.

PROSITE; PS5011; PROTEIN, KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYCLASE ACTIVITY ON BINDING OF ANF. SEEMS TO BE STIMILATED MORE EFFECTIVELY BY BRAIL NATRIURETIC PEPTIDE (HAN GUANYLATE: CYCLASE ACTIVITY ON BINDING OF ANF. SEEMS TO BE STIMILATED MORE EFFECTIVELY BY BRAIL NATRIURETIC PEPTIDE (BNP) THAN BY ANP.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- MISCELLAREOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CICALARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.

-1- SIMILARITY: BELONGS TO ADENYLY: CYCTATION.
  TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DISULFID
                                                                                    SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The primary structure demonstrates diversity Cell 58:1155-1162(1989)
                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                        DOMAIN
                                                                                                               Receptor; Trans
cGMP synthesis;
                                                                                                                                                                                                                                                                             InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_receptorN.
                                                                                                                                                                                                                                                                                                             InterPro; IPR001828; ANF_receptor. InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
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Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-8937656;
                                                                                                                                                                                                                                                                                                                                                    PIR; A33300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B-type receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atrial natriuretic
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16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANPB_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   M26896; AAA41205.1; -.
                                                                                                                                                                                                                                                                                                                                         Q02846;
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an email to license@isb-sib.ch).
                                                                                                                              Transmembrane;
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861
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14, Last sequence update)
40, Last sequence update)
c peptide receptor B precursor (ANP-B) (ANPRB) (GC-B)
e) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide
  22
1047
458
478
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786
991
101
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S., Bellet R.A.,
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                                                                                                                            Glycoprotein;
ATRIAL NATRIURETIC PEPTIDE EXTRACELLULAR (POTENTIAL). POTENTIAL. (CYTOPLASMIC (POTENTIAL). PROTEIN KINASE-LIKE. GRANYLATE CYCLASE. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasma
in this
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RESULT 15
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DISULFID
CARBOHYD
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CARBOHYD
                                                         MEDLINE-91056089; PubMed-1978722;
Yamaguchi M., Rutledge L.J., Garbers I
"The primary structure of the rat guar
natriuretic peptide receptor gene.";
J. Biol. Chem. 265:20414-20420(1990).
                                                                                                                                                                                                                                                                                                                                          ANPA_RAT
P18910;
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial
                                                                                                                                                Chinkers M., Garbers D.L., Cha
Goeddel D.V., Schulz S.;
"A membrane form of guanylate
peptide receptor.";
            Duda T., Goracz
"Site-directed
                               SEQUENCE FROM N.A MEDLINE-91352095;
                                                                                                                                   peptide receptor.";
Nature 338:78-83(1989).
                                                                                                                                                                                                                                        Eukaryota;
Mammalia; F
                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                     MEDLINE-89143770;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Goraczniak R.M., Sharma R.K.; rected mutational analysis of a membrane guanylate cyclase eals the atrial natriuretic factor signaling site.";
                                                                                                                                                                                                                                       Eutheria;
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                                                                                                                                                                           pubMed=2563900;
ers D.L., Chang M.S.,
                               PubMed=1679239
                                                                                                                                                                                                                                                           (Rat)
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448
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161
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Rodentia;
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41.9%;
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Pred. No. 2.
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                                                                                                                                                       cyclase
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S062C4922BCC14A3 CR
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l natriuretic peptide
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Murinae; Rat
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Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00255; NATPEPTIDER.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00044; CYCC; 1.
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PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X14773; CAA32881.1; -.
EMBL; J05677; AAA41200.1; -.
EMBL; M74535; AAA41202.1; -.
EMBL; S03348; OYRTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; Trans cGMP synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_receptorN.
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               423 DGLKKRL----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q02846;
                                                                              Similarity
DNLLSRMEQYANNLEELVEERTQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFD 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein; Phosphorylation; Lyase
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FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE
                                                              40;
                                                                                                                                                                                                                N-LINKED
N-LINKED
                                                              Score 457.5; DB 1; Pred. No. 3.9e-24; 0; Mismatches 78;
                                                                                                                                                N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
Q -> H (IN REF. 3).
L -> P (IN REF. 3).
                                                                                                                                                                                                                                                                INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
N-LINKED (GLCNAC. . .)
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BY SIMILARITY.
BY SIMILARITY.
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POTENTIAL.
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b (GLCNAC...)
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c (GLCNAC...)
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990 LFGDTVNTASRMESNGEALKIHLSSETKAVLEEFDGFELELRGDVEM 1036	596 LFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREEL 642	930 PYRNGQLHAREVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVVGLKMPRYC 989	539 H-KESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYC 595	870 SVTIYFSDIVGFTALSAESTPMQVVTLLNDLYTCFDAVIDNFDVYKVETIGDAYMVVSGL 929	479 NYTMLESDIVGETAICSQCSPLQVITMLNALYTREDQQCGELDVYKVETIGDAYCVAGGL 538

Search completed: June 27, 2003, 13:03:26 Job time: 13.0695 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07; Search time 9.93048 Seconds
(without alignments)
2585.358 Million cell updates/sec

US-09-762-767A-4 3231

Title: Perfect score: Sequence: 1 MYGFVNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	221	Result No.
987 987 916 909.5 909.5 793 789.5 779.5 481.5 453.5 453.5 433.5 433.5 428.5 433.5 428.5 433.5 434.6 435.5 435	3231 3206	Score
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gallus gall	homo sapien	dictyosteli	drosophila	mus musculu	homo sapien	xenopus lae	homo sapien	rattus norv	bos taurus	mycobacteri	cavia porce

ALIGNMENTS

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Matches 619
CYG1_BOVIN
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01-APR-1990 (Re
16-OCT-2001 (Re
Guanylate cycla
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Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

LYASE; CGMP Synthesis; Alternative splitcing.

DOMAIN
421
554
GUANYLATE CYCLASE.

VARSPLIC
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425
MISSING (IN ISOFORM HSGC-2).

SEQUENCE 619 AA; 70514 MW; 231E4E660DE02AA1 CRC64.
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(Rel. 14, Created)
(Rel. 14, Last sequence update)
(Rel. 40, Last annotation update)
yclase soluble, beta-1 chain (EC 4
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                             STANDARD;
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Query Match
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Matches 61
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PIR; S0.653; OYBO70.

PDB; 1AWN; 28-JAN-98.

InterPro; IPRO01054; G_Cyclase.

Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS000452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.

LYase; CGMP synthesis; 3D-structure.

DOMAIN 421 554 GUANYLATE CYC
SEQUENCE 619 AA; 70502 MW; BEFB14952BE
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GUCYIB1 OR GUCIB3 OR GUCB3.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Proc. Natl. Acad. Sci. U.S.A. 94:13414-1341-1-CATALYTIC ACTIVITY: GTP = 3',5'-cyclic-1-ENZYME REGULATION: ACTIVATED BY NITRIC MAGNESEIOM OR MANGANESE IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The primary structure of t guanylate cyclase."; FEBS Lett. 239:29-34(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE-Lung; MEDLINE-89031214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koesling D., Herz J
Muelsch A., Boehme
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NCBI_TaxID=9913;
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MEDLINE=98054247; PubMed=9391039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation: European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way liftled and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: CYCOPLASMIC.
TISSUE SPECIFICITY: LUNG AND BRAIN.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL
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MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
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cDa subunit
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A Nakane M., Saheki S., Kuno T., Ishii K., Murad F.;

A Nakane M., Saheki S., Kuno T., Ishii K., Murad F.;

A Nakane M., Saheki S., Kuno T., Ishii K., Murad F.;

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                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-1 chain (EC 4
(Soluble guanylate cyclase small subunit).
GUCY1B1 OR GUCY1B3 OR GUC1B3.
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    EMBL; M22562; AAA41204.1;
PIR; A31871; OYRTB1.
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                                CYG2_RAT STANDARD; PRT; 682 AA. P22717; 01-AUG-1991 (Rel. 19, Created) 01-AUG-1991 (Rel. 19, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Guanylate cyclase soluble, beta-2 chain (EC 4. GUCY1B2.
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Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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DOMAIN 408 536
SEQUENCE 682 AA; 76196 MW;
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InterPro; IPR001230; Prenyl_site.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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MEDLINE-91105012; PubMed-1980215;
Yuen P.S.T., Potter L.R., Garbers
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TISSUE SPECIFICITY: KIDNEY AND LIVER.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CY
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GU
FAMILY.
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           413
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                                                                                                                                        SCQLERKKEELRVLSNHLAIEKKKTETLLYAMLPEHVANQLKEGRKVAAGEFETCTILFS
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AACE-PIQIVNMLNSMYSKFDRLTSVHD--
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Pred. No. 1.4e-60;
4; Mismatches 195
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CYG2_HUMAN
075343; Q9N
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EMBL; AF218383;
HSSP; P19687; 1A
InterPro; IPR001054; G_cyclase.
Pfam; PF00311; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      075343; Q9NZ64;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Courted the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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and D13S155 ".
                                                                                                                             MIM; 603695;
                                                                                                                                                    Genew;
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Scholz H., Eiberg H.;
"Assignment of GUCYIB2, the gene coding for the beta2 subunit
"Assignment of GUCYIB2, the gene coding for the beta2 subunit
guanylyl cyclase to chromosomal band 13q14.3 between markers I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The beta(2) subunit of soluble guanylyl cyclase contains human-specific frameshift and is expressed in gastric card Biochem. Biophys. Res. Commun. 271:64-69(2000).
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MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL
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                                                                                                                                                                                                 AF038499; AAD09440.2; AF218383; AAF66105.1;
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16-OCT-2001 (Rel. 4
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SEQUENCE
                                                                                                            SEQUENCE FROM N.A.
STRAIN-Wistar Kyoto; TISSUE-Aorta;
MEDLINE-20571097; PubMed-11121588
                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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llarity 36.6%;
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40, Last sequence update)
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Rodentia;
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Pred. No. 1.6e-
96; Mismatches
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                                                                                                                                                                                               Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00452; GUÀNYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_L
Lyase; cGMP synthesis; Multigene family
DOMAIN 519 646 GUANYLATE (
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Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CY
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
598
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                                                                                                                                                   KTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVN
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SEEVLTPDGRPIQMRIGIHSGSVLAGVVGVRMPRYCLFGNNVTLASKFESGSHPRRINIS
                                                                    MLNELYTRFD----
                                                                                                                                   KTVDLLYSIFPGDVAQQLWQRQQVQARKFDDVTMLFSDIVGFTAICAQCT----PMQVIS
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. No. 1.2e-55;
ismatches 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --
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in no way
commercial
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EYTYRCLMSPENS ||: |: |:| PTTYQ-LLKREDS

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Behrends S., Harteneck C., Schultz G., Koesling D.;

A variant of the alpha 2 subunit of soluble guanylyl cyclase grand functions as a dominant negative protein.";

contains an insert homologous to a region within adenylyl cyclases and functions as a dominant negative protein.";

L. J. Biol. Chem. 270:21109-21113(1995).

C. I- FUNCTION: HAS GUANYLYL CYCLASE ON BINDING TO THE BETA-1 SUBUNITS COLOR REGULATOR OF GUANYLYL CYLASE ACTIVITY AS IT FORMS NON-FUNCTION HETERODIMERS WITH THE BETA SUBUNITS.

C. I- CATALYIK ACTIVITY: GTP - 3',5'-cyclic GMP + diphosphate.

C. I- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN FETAL BRAIL SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C. I- SUBCELLOUAR LOCATION: Cytoplasmic.

C. I- SUBCELLOUAR LOCATION: Cytoplasmic.

C. I- SUBCELLOUAR LOCATION: Cytoplasmic.

C. I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-2 (SHOWN HERE) AND ALPHA-2-1; ARE PRODUCTS: 2 ISOFORMS; ALPHA-2 (SHOWN HERE) AND ALPHA-2-1; ARE PRODUCTS: 2 ISOFORMS; WHILE THE ALPHA-2-1 FORM IS EXPRESSED IN FETAL BRAIL LIVER, COLON AND ENDOTHELIUM.

C. I- MISCELLANDOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUTIONS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

C. I- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE.
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01-FEB-1994
16-OCT-2001
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PROSITE: PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS0125; GUANYLATE_CYCLASES_2;
Lyase; CGMP synthesis; Multigene family
DOMAIN 521 648
DOMAIN 51 76 ALA-RICH.
DOMAIN 51 58 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92070494; Pubmed-1683630; Wedel B., Koesling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-2 chain (EC
GUCYIA2 OR GUCIA2 OR GUCSA2.
                                                                                                                                                                                                                                                                                           EMBL; X63282; CAA44921.1;
EMBL; Z50053; CAA90393.1;
PIR; S18325; S18325.
HSSP; P19687; IAWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       guanylyl cyclase.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                            Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                            MIM; 601244;
                                                                                                                                                                                                                                                                        Genew;
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                        Multigene family; Alternative GUANYLATE CYCLASE. ALA-RICH.
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P19686;
01-FEB-1991
                                                                                                                                                                               01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC
(Soluble guanylate cyclase large subunit).
GUCY1A1 OR GUC1A1.
                        Nakane M., Arai K., Saheki S., Kuno T., Bue "Molecular cloning and expression of cDNAs guanylate cyclase from rat lung.";
J. Biol. Chem. 265:16841-16845(1990).
  SEQUENCE
                                                                            MEDLINE=91009100;
                                                                                         TISSUE-Lung;
                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                      Rattus norvegicus (
Eukaryota; Metazoa;
                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                            Mammalia; Eutheria;
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Sciurognathi; Muridae;
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MEDLINE-97151325; pubMed-8997507;

Smigrodzki R.M., Levitt P.;

Smigrodzki R.M., Levitt P.;

The alpha 1 subunit of soluble guanylyl cyclase is prenatally in the rat brain.";

Brain Res. Dev. Brain Res. 97:226-234(1996).

-i- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + dip.

-i- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + dip.

MAGNESIUM OR MANGANESE IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M57405; AAA41206.1; -. EMBL; U60835; AAB17953.1; -. PIR; A38297; OYRTA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyase; cGMP synthesis; Multigene family.

DOMAIN 480 607 GUANYLATE CYCLASE.
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InterPro; IPR001054; G_cyclase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 1.
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SUBCELLGUAR LOCATION: CYCOPLASMIC.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLIFORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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FTAICSQCS----PLQVITMLNALYTREDQQCGELD--
                                              FNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPC
                                                                                               GKLKATLEHAHQALEEEKKKTVDLLCSIFPSEVAQQLWQGQIVQAKKFNEVTMLFSDIVG
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"Human soluble guanylate cyclase: functional expression and revisionaryme family.";

It soenzyme family.";

Biochem. J. 335:51-57(1998).

C -!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

C -!- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE MAGNESIUM OR MANGANESE IONS.

C -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C -!- SUBCELLULAR LOCATION: Cytoplasmic.

C -!- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOL FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

C -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCL
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01-JUL-1993 (Rel. 26, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)
(Soluble guanylate cyclase large subunit) (GCS-alpha-3).
GUCY1A1 OR GUCY1A3 OR GUCLA3 OR GUCSA3.
                                                                                                  This SWISS-FROM THE SWISS Institute of Bioinformatus between the Swiss Institute of Bioinformatus the European Bioinformatics Institute. There were a proposed to the statement is not removed entities requires a license agreement (See entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Kidney;
Gansemans Y., Brouckaert P., Fiers W.;
"Human soluble guanylate cyclase large subunit mRNA,
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92316204; PubMed-1352257; Giuili G., Scholl U., Bulle F., Guellaeen G. "Molecular cloning of the cDNAs coding for t. soluble guanylyl cyclase from human brain."; FEBS Lett. 304:83-88(1992).
                          EMBL; X66534; CAA47145.1; -. EMBL; U58855; AAB94794.1; -. EMBL; Y15723; CAA75738.1; -. PIR; S23098; S23098.
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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Mammalia; Eutheria;
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                                                                                                                      . Usage by and for http://www.isb-sib.
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RESULT 10
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Best Local (
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CYG3_BOVIN STANDARD;
CYG3_BOVIN STANDARD;
P19687;
P19687;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
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CONFLICT
CONFLICT
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SMART; SM00044; CYCC; 1.

PROSITE; PS00452; GUANYLATE CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

Ivase; cGMP synthesis; Multigene family.

GUANYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 1.
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                                                                                                                                          TSRTETTGEKGKINVSEYTYRCL------MSPENSDPQFHLEHRG
                                                                                                                                                                                                       TAICSQCS----PLQVITMLNALYTRFDQQCGELD---VYKVETIGDAYCVAGGLHKESD
                                                                                                                                                                                                                                               EDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVTQCGNAIYRVLPQLQ-PGNCSL
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                                                                                                                       ANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPG
                                                                                                                                                                                  HHARSICHLALDMMEIAGQV-QVDGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNL
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VIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFSTLLK
QSSHCQEAGKRGR -> LSKNLLVKRFLKYVTRKMKTSLGW
LEAPLKIFKQLQYPSETEQPLPRSRKKGQ (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 789.5;
Pred. No. 5.
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GDAYCYA -> AMPIWH (IN REF. 1).

GNANFLYKASGID -> ASOPERQSIRNRLATYIPIYKSLG

FDSLKMCRASESTLGIVDG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DA1E14A5E11451CF CRC64;
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Schultz G., Boehme
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MEDLINE-90306336; PubMe
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MEDLINE MODELING OF 472-628.
MEDLINE=98054247; PubMed=9391039;
Liu. Y., Ruoho A.E., Rao V.D., Hurley
"Catalytic mechanism of the adenylyl
and mutational analysis.";
Proc. Natl Acad Control
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                    "The primary structure of the larger subunit of soluble cyclase from bovine lung. Homology between the two subur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Boyinae; Bos.
s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

Lyase; cGMP synthesis; Multigene family; 3D-structure.

DOMALN 482 609 GUANYLATE CYCLASE.

SEQUENCE 691 AA; 77532 MW; 5D1FE4D2204E8683 CRC64; InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1. EMBL; X54014; CAA37960.1; PIR; S10713; OYBO77. PDB; 1AWN; 28-JAN-98. CRC64;

KEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEIL-QMFGKMFFVFCQESGYDT -FHQDCREFVDQPCELYSVHIRSARPHPPPGKPVSSLVIPASLFCKTFPFHFMLDRDMSI DFYEDLDRFEENGTQ-------LILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFLIEEKESKEE ILRVLGSNVREFLQNLDALHDHLATIYPGMRAPSFRCTDAEKGKG-----KENRKSLEREDFEKIVVDQA-----IAAGVPV-----EIIKESLGEELFKICYEED-EY VLYVYYFFPKRITSLILPGIIKAAARILYETEVEVSSTPSR ILGVVGGTLKDFLNSFSTL--------ESRISPYT-FCKAFPFHIIFDRDLVV -LKQSSHCQEAEK-KGRFEDASILCLDKDPD 151 189 299 229 240

90;

Score 770; Pred. No. 1 Mismatches

DB 1; ..3e-45;

Length

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Indels

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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Head-specific guanylate cyclase (EC 4.6.1.2).
GYC-ALPHA-99B oR GYC-ALPHA-9BA OR GYC OR DCC1.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach
Insecta; Enhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROME
                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    "Isolation of a Drosophila gene encoding a head-specific guar cyclase.";
J. Neurochem. 60:1570-1573(1993).
-I- FUNCTION: MAY HAVE A ROLE IN PHOTOTRANSDUCTION. A SECOND
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Canton-S; TISSUE-Head;
MEDLINE-93203896; PubMed-8095978;
                                                                                                                                                                                                                                                                                                          Yoshikawa S., Miyamoto Mikoshiba K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYGH_DROME
                         EMBL;
                                                                                                                                                              MAY BE REQUIRED FOR ENZYME ACTIVITY.

CATALTYTC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

SUBUNIT: DIMER (PROBABLE).

SUBCELLULAR LOCATION: Cytoplasmic (Potential).

TISSUE SPECIFICITY: HEAD, WHERE IT IS PREFERENTIALLY EXPRESSED IN THE CNS AND THE RETINA. NOT FOUND IN BODIES.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE.
 ; S57126; AAB25820.1;
JH0810; JH0810.
; P19687; IAWN.
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                                                                                                                                                                                                                                                                                                                       I., Aruga
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                                                                                                                                                                                                                                                                                                                      J.,
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NPR1 OR ANPRA.
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RESULT 12
ANPA_HUMAN
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Best Local :
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PROSITE: PS00452; GUANYLATE_CYCLASES_1; FALSE_N
PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.

Lyase; cGMP synthesis; Multigene family; Vision
DOMAIN 465 591
GUANYLATE CYCLASE.
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Atrial natriuretic peptide receptor A precursor (Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial
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Pfam; PF00211; guanylate_cyc;
SMART; SM00044; CYCc; 1.
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; Metazoa; Eutheria;

Chordata; Primates;

Craniata; Vo Catarrhini;

Vertebrata;
i; Hominidae;

Euteleostomi;

(ANP-A) (ANPRA) (GC-A) natriuretic peptide

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Lee Buropean Block.

use by non-profit institute.

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Cell. Mol. Neurobiol. 14:1-7(1994).
-1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC
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Takahashi Y., Nakayama T., Soma M., Izumi Y., Kanmatsuse K.;
"Organization of the human natriuretic peptide receptor A gene.";
Biochem. Blophys. Res. Commun. 246:736-739(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 634-1048 FROM N.A.
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"Identification of func
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CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP +
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MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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AB010472;
AB010474;
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AB0104777;
AB0104779;
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PTODOM; PD000001; Euk_pkinase; 1.
SMART; SM00044; CYGC; 1.
PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
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DOMAIN
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EMBL; AF190631; AAF013440.1;
EMBL; S72628; AAD14112.1;
PIR; S04459; OYHUAR.
HSSP; O02846; IAWL.
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Pfam; PF00211; guanylate_cyc;
Pfam; PF01094; ANE_receptor; 1
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MIM; 108960;
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InterPro; IPR000719; Euk_Pkinase.
InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_receptorN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthesis;
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
    TRRGLYLSDIPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50125; GUANYLATE_CYCLASES_PS50011; PROTEIN_KINASE_DOM;
                                           ITDYGLESFRDLDPE-
                                                                                              DWMFRYSLTNDIVKGMLFLHNGAICS
                                                                                                                                                       IEL-
                                                                                                                                                                               EECDHTQFLIEEKESKEEDFYEDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVT
                                                                                                                                                                                                                                     GMRAPSFRCTDAEKGK--GLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRN
                                                                                                                                                                                                                                                                LALVGSLSLLGILIVSFFIYRKMQLEKELASELWRVRWEDVEP-----SSLERHL-----
                                                                                                                                                                                                                                                                                        LQMFGKM-----FFVF----CQESGYDTILRVLGSNVREFLQNLDALHDHLATIYP
                                                                                                                                                                                                                                                                                                                   ENGAFRYVLNYNGT-SQELVAVSGRKLNWPLGYPPPDIPKCGFDNEDPACNQDHLSTLEV
                                                                                                                                                                                                                                                                                                                                              EEGQFLVRIIYDDSKTYDLVAAASKVLN-----------LNAGEI 66
                                                                                                                                                                                                           --RSAGSRLTLSGRGSNYGSLL----TTEGQFQV---FAKTAYYK--GNLVAVKRVNRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                         larity 27.7%;
Conservative
                                                          -GLLDVEKLECEDELTGTEISCLRLKGQMIY---LPEADSILFLCSPSV--MNLDDL
                                                                                                                                                      TRKVLFELKHMRDVQNEHLTRFVGACTDPPNICILTEYCPRGSLQDILENESITL
                                                                                                                         QCGNAIYRVLPQLQPGN-CSLLSVFSLVRPHIDISFHGILSHINTV----FVLR
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27.78;
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-HDATRDL-----
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CYTOPLASMIC
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INTERCHAIN (PROBABLE).
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No. 1.1
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GGLCNAC...

GGLCNAC...
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  -VLLGEQ--FREEYKLTQELEIL---
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RESULT 13
               CYCLASE ACTIVITY ON BINDING OF ANF.

-!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THESE AND RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
-!- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
-!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                 MEDILINE-91352095; PubMed-1679239;
Duda T., Goraczniak R.M., Sharma R.K.;
"Site-directed mutational analysis of a membrane guanylate cyclase cDNA reveals the atrial natriuretic factor signaling site.";
Proc. Natl. Acad. Sci. U.S.A. 88:7882-7886(1991).
-1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLANGED CONTROL NATRIAL NATRIURETIC PERTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                    Goeddel D.V., Schulz S.;
"A membrane form of guanylate cyclase peptide receptor.";
Nature 338:78-83(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
                                                                                                                                                                                                                                                                                              Yamaguchi M., Rutledge L.J., Garbers D.L.;
"The primary structure of the rat guanyly!
natriuretic peptide receptor gene.";
J. Biol. Chem. 265:20414-20420(1990).
                                                                                                                                                                                                                                                                                                                                            MEDLINE-91056089; PubMed-1978722;
Yamaguchi M., Rutledge L.J., Garb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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01-NOV-1990
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Rodentia;
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Sciurognathi;
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; Murinae; Rattus.
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InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_recepfam; PF00069; pkinase; 1
Pfam; PF00211; guanylate_cyc; 1
Pfam; PF01094; ANF_receptor; 1
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PTODOM; PD000001; EUK_PKINASE; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS00458; ANE_RECEPTORS; 1.

PROSITE; PS00452; GGANYLATE_CYCLASES_1;

PROSITE; PS50125; GUANYLATE_CYCLASES_2;

PROSITE; PS50111; PROTEIN_KINASE_DOM; 1.
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the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
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EMBL; J05677; AAA41200.1; -.
EMBL; M74535; AAA41202.1; -.
PIR; S03348; OYRTR.
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112; Conserv
                                                                                                                                               VVSGLP---VRNGQLHAREVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVV
                                                                                   GQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLEHRGPVSMK
                                                                                                                                                                                                TVSGLPEPCIH----HARSICHLALDMMEIAGQVQV---DGESVQITIGIHTGEVVTGVI
                                                                                                                                                                                                                                                                        TIYFSDIVGFTALSAEST----PMQVVTLLNDLYTCFDAVID---NFDVYKVETIGDAYM
                                                                                                                                                                                                                                                                                                                            TILESGIVGENAECSKHASGEGAMKIVNLLNDLYTREDTLIDSRKNPEVYKVETVGDKYM
                                                   GLKMPRYCLFGDTVNTASRMESNGEALKIHLSSETKAVL--
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IPR000719;
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Euk_pkinase.
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Pred. No. 1
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GUANYLATE CYCLASE.
BY SIMILARITY.
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1.6e-24;
hes 82;
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RECEPTOR

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RESULT 14
ANPA_MOUSE
 Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00255; NATPEPTIDER.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM0044; CYCC; 1.
SMART; SM0044; CYCC; 1.
PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00459; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95139994; PubMed-7838126; Schoenfeld J.R., Sehl P., Quan C., Burn Ragonist selectivity for three species receptor-A.";
                                                                                                                                        MGD; MGI:97371; Npr1.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR00719; Euk_pkinase.
InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_receptorN.
                                                                                                                                                                                                                            EMBL; J05504; AAA37670.1; -.
EMBL; L31932; AAA6945.1; -.
PIR; A36568; OYMSAR.
PIR; A33088; A33088.
HSSP; Q02846; IAWL.
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NPRI OR NPRA.

Mus musculus (Mouse).

                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pandey K.N., Singh S.; "Molecular cloning and expression of murine guanylate cyclase/atrial natriuretic factor receptor cDNA."; J. Biol. Chem. 265:12342-12348(1990).
                                                                                                                                                                                                                                                                                                                             entities requires a license agreement or send an email to license@isb-sib.ch
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16-OCT-2001
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NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANF.
CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWAITH GUANYLATE CYCLASE ACTIVITY (AMP-A AND ANP-B) AND ONE (AMP-CWITCH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AMP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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iuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
                                                                                                                              pkinase;
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Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthesis;
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NAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCI
                                                FNKENSSNI - - - -
                                                                                                                                                                                          LSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTEISCLRLKGQM
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                                                                                                                            IYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEQFREEYKLTQELE
                                                                                                                                                            -----FRPSMDLQ-----SHLEELGQL------MQRCWAEDPQERPPFQQIRLALRK
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                                 -EEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGF
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BY SIMILARITY.
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INTERCHAIN (PROBABLE).
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P16067;
01-APR-1990
                    Pfam;
Pfam;
                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-89376566; Pul Schulz S., Singh S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide
                                                                                                                                                    EMBL;
                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B-type receptor)
                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                             InterPro;
                                                                                           InterPro;
                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                   DEFENCTIVELY BY BRAIN NATRIURETIC EPPTIDE. HAS GUANYLATE CYCLASE ACTIVITY GUA BY AND ONE CATALYTIC ACTIVITY:

SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND ONE (AMP-C) MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND ONE (AMP-C)
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SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLAS
                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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                                                                                                                                     A33300; OYRTBR.
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                  PF00211;
PF01094;
                                                       Q02846; 1AWL.

Pro; IPR001828; ANF_receptor.

Pro; IPR000719; Euk_pkinase.

Pro; IPR001054; G_cyclase.

Pro; IPR001170; Ntpep_receptorN.
                                                                                                                                                    M26896;
                                                PF00069;
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               pkinase; 1.
guanylate_cyc; 1.
ANF_receptor; 1.
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S., Bellet R.A.,
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PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
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RCLMSPENSDPQFHLEHRGPVSMKGKKEPMQVWFLSRK
                                         RHRPHDQLRLRIGVHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGQALKIHVSSTTK
                                                                                                                       YTREDTLTDSRKNPFYYKVETYGDKYMTYSGLP-EPCIHHARSICHLALDMMEIAGQVQV
                                                                                                                                                                                LYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLNLNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVR-EFLQ--NLDALHDHLATIYPG
                                                      ---DGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTY 569
                                                                                                                                                              LYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAEST----PMQVVTLLNDL
                                                                                                                                                                                                                        TERPDFGQIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLVEERTQAYLEEKRKAEAL
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27.98;
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BY SIMILARITY.
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    Phosphorylation;

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114

512

833 393 773 357 717 304 657 277 597

Search completed: June 27, 2003, 13:03:29 Job time: 12.9305 secs

1007 DAL----DELGCFQLELRGDVEMKGKGKMRTYWLLGER 1040

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OM protein - protein search, using sw model
                                                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: June 27, 2003, 13:00:58; Search time 31.2101 Seconds (without alignments) 4086.601 Million cell updates/sec

Title: Perfect score: US-09-762-767A-4 3231

Sequence:

1 MYGFVNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_archea:*
sp_bacteria:*
sp_fungi:*

sp_phage:* sp_organelle:*

sp_plant:*
sp_rodent:* sp_virus:*

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	_	Result
914	929.5	938	955	955	960.5	983	1105	1761	1870.5	1883	1883	1903.5	2859	2887	3198	Score
28.3	28.8	29.0	29.6	29.6	29.7	30.4	34.2	54.5	57.9	58.3	58.3	58.9	88.5	89.4	99.0	Query Match
699	690	751	940	686	. 685	636	742	649	604	787	758	600	617	614	620	Length DB
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Q17707	Q9VFC5	002298	076340	P92006	Q9XTE0	092001	Q91xJ7	Q17010	Q95NK5	Q9VA09	Q24086	077106	Q90VY5	P79998	054865	ID
Q17707 caenorhabdi	Q9vfc5 drosophila	002298 caenorhabdi	076340 manduca sex	P92006 caenorhabdi	Q9xte0 caenorhabdi		Q91xj7 rattus norv	Q17010 anopheles g	Q95nk5 hemicentrot	Q9va09 drosophila	Q24086 drosophila	077106 manduca sex		P79998 oryzias lat	O54865 mus musculu	Description

Query Match

99.0%; Score 3198;

DB 11; Length 620;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
456.5	458	464	466	467.5	469.5	470	471	472	478.5	490.5	493	565	646.5	685	701.5	704.5	720	726	729.5	757	778	778	778	783	786.5	788	788	912.5
14.1	14.2	14.4	14.4	14.5	14.5	14.5	14.6	14.6	14.8	15.2	15.3	17.5	20.0	21.2	21.7	21.8	22.3	22.5	22.6	23.4	24.1	24.1	24.1	24.2	24.3	24.4	24.4	28.2
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	Q9vf19 drosophila	Q9pwh0 xenopus lae	Q91x04 mus musculu	a	Q90yb7 rana catesb	Q18331 caenorhabdi	oryzias	Q98uil oryzias lat		093490 anguilla ja	4		P90895 caenorhabdi							3	Q9erl9 mus musculu	mus mus	P79997 oryzias lat		Q8tah3 homo sapien	Q90vv5 fugu rubrip	Q9nnw8 homo sapien	Q9bi80 caenorhabdi

ALIGNMENTS

ONDER REPORTED TO SERVICE OF SERV
O54865; PRELIMINARY; PRT; 620 AA. O54865; O1-UN-1998 (TREMBLrel. 06, Created) O1-UN-1998 (TREMBLrel. 06, Last sequence update) O1-UN-1998 (TREMBLrel. 20, Last sequence update) SOluble guanylate cyclase beta-1 subunit. GUCYIB3 OR GC-S-BETA-1. EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus (Mouse). EUKARYOTA; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. MCBL_TAXID-10090; [1] TISSUE-LUNG; SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAING-1997) to the EMBL/GenBank/DDBJ databases. [2] SEQUENCE FROM N.A. STRAING-1984516; PubMed-10984516; STRAING-19984516; Sharina I.G., Krumenacker J.S., Martin E., Murad F.; "Genomic organization of alpha 1 and beta 1 subunits of the mammalian proc. Natl. Acad. Sci. U.S.A. 97:10878-10883(2000). EMBL; AP297083; AAG17447.1; EMBL; AP297083; AAG17447.1; EMBL; AP297083; AAG17447.1; EMBL; AP297083; AAG17447.1; EMBL; AP297083; AG17447.1; SMART; SM00044; CGC; I. PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1. PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1. EXECUENCE 620 AA; 70597 MW; EED89ABF339F4EF9 CRC64;

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                                                  x MEDLINE-98237571; PubMed-9578459;
x Mikami T., Kusakabe T., Suzuki N.;
**Molecular cloning of cDNAs and exprebeta subunits of soluble guanylyl cyc.
latipes.";
Eur. J. Biochem ~~~
                                                                                                                                                                              D P79998 PRELIMINARY; PRT; 614 AA.

C P79998;
C P79998;
T 01-MAY-1997 (TrEMBLrel. 03, Created)
T 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
T 01-MAY-1997 (TrEMBLrel. 20, Last annotation update)
Soluble guanylyl cyclase beta subunit (EC 4.6.1.2).
S Oryzias latipes (Medaka fish).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
C Eukaryota; Metazoa; Chordata; Percomorpha; Atherinomorpha;
C Acanthomorpha; Acanthopterygil; Percomorpha; Atherinomorpha;
C Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
N NCB_TaxID-8090;
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                   SEQUENCE FROM N.A. MEDLINE=99303623;
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Best Loc
Matches
Q90VY5 PRELIMINARY; PRT; 617 AA.
Q90VY5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Soluble guanylyl cyclase betal subunit.
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Mikami T., Kusakabe T., Suzuki N.;
"Tandem organization of medaka fish sol
and beta1 subunit genes. Implications f.
two subunit genes.";
J. Biol. Chem. 274:18567-18573(1999).
EMBL; AB002850; BAA19199.1;
EMBL; AB022281; BAA76691.1;
HSSP; P16068; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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VWFLSRKNTGTEE
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PS00452; GUANYLATE_CYCLASES.
PS50125; GUANYLATE_CYCLASES.
                               POLOPGNCSILSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVÉKLECEDELTGTE
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Pred. No. 9
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submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB062172; BAB60908.1; -.

EMBL; AB062170; BAB60906.1; -.

RINTERPO; IPR001054; G_Cyclasse.

RINTERPO; IPR0001054; G_Cyclasse.

RINTERPO; IPR0001054; G_Cyclasse.

RINTERPO; IPR0001054; G_Cyclasse.

RPGSITE; PS00112; GABDXYPEPT_ZN.1; UNKNOWN_1.

RPGSITE; PS00112; GABDXYPEPT_ZN.1; UNKNOWN_1.

RROSITE; PS00125; GGANYLATE_CYCLASSES_1; UNKNOWN_1.

PROSITE; PS00125; GGANYLATE_CYCLASSES_2; 1.

SEQUENCE 617 AA; 70236 MW; 7B531B5896A06191 CRC64;
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Frugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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                                        CLFGNTVNLTSRTETTGEKGRINVSEFTFRCLQSAENADPQFHLEYRGPVTMKGKKEPMK
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Pred. No. 1.3e-207;
1; Mismatches 28;
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MEDLINE-98409773; PubMed-9736646;

Nighorn A., Gibson N.J., Rivers D.M., Hildeb

"The nitric oxide-cGMP pathway may mediate c
sensory afferents and projection neurons in
manduca sexta.";
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01-NOV-1998 (TIEMBLEL 08, Created)
01-NOV-1998 (TIEMBLEL 08, Last sequence update)
01-NOV-1998 (TIEMBLEL 20, Last annotation update)
01-MAR-2002 (TIEMBLEL 20, Last annotation update)
soluble guanylyl cyclase beta-1 subunit.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Disphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
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EMBL; AF062751; AAC61264.1; -.
HSSP; P16068; IAWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
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Pred. No. 2.1e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7F7D0136E6ADACB9 CRC64;
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e-135;
138;
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Query Match
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Matches 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Two Drosophila genes that encode the alph brain soluble guanylyl cyclase."; J. Biol. Chem. 270:15368-15376(1995). EMBL; U27123; AAA87941.1; -. HSSP; P16068; IAWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0013973; Gyc-beta-100B.
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera;
Ephydroidea; Drosophi
NCBI_TaxID=7227;
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371; Conserv
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           ELTGTEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVL
                                                 AVSRVIPRVAEENCSLIEVVEAIRPHLQLNFENILSHINTIYVLQTRQGAMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYGFVNYALELLVLKHFGEEIWEKIKKKAMVSMEGQFLVRQIYDDEITYNLIGAAVEILN
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                                                                                    AIYRVLPQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECED
                                                                                                                          EINVAAKSQVDAKKDEVPDDMEFL----CEAPLISPATFCKVFPFHLMFDRQMKIVQAGK
                                                                                                                                                                                                                                                                                RAIARENQQLLEDAVATTTTGSATVVLAPSSDAERNNHHNGSNGSNNNGMANNGNTVNVN
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Mismatches 12
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.;
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shie B.C., Siden Fiamos I., Simpson M., Skupski M.P., Smith T.,
RA Siden R., Simbon M., Shipson M., Skupski M.P., Smith T.,
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GYC-BETA-100B OR GYCBETA100B OR CG1470.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;

Ephydroidea; Drosophilidae; Drosophila.
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KRYDNYTLMFSGIVGFGQYCAANTDPDGAMKIVKMLNELYTVFDALTDSKRNLNVYKVET
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(TrEMBLrel. 13, Last seq
(TrEMBLrel. 20, Last ann
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EMBL; AE003777; AAF57119.1; -. HSSP; P16068; 1AWN.
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InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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KRYDSYTLMFSGIVGFGQYCAANTDPDGAMKIVKMLNELYTVFDALTDSKRNLNYYKVET
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KPTPMDCWFLTRATSSILGGTSST
                    KKEPMQVWFLSRKNT----
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Pred. No. 1.1e-133;
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EMBL; AB062387; BAB58877.1; JOINI
EMBL; AB062388; BAB58877.1; JOINI
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EMBL; AB062389; BAB58875.1; -..
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
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Q95NK5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Soluble guanylyl cyclase betal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanabe Y., Suzuki N.;
"Genomic Structure and
Cyclase beta Subunit Ge
Submitted (MAY-2001) to
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00211; guanylate_cyc; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
SEQUENCE 604 AA; 68198 MW; B1C79618705934D2 CRC64;
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                TVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQQQVDGESVQITIGIHTGEVVTGVI
                                                                              AKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVE
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TVGDKYMAVSGLPVPCADHAKCIAKMALEMKELSADVIMEGDPIVITIGVYSGEVVTGVV
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                                                              AKKFECYTLMFSGIFGFGDFCRRYS--HDAMKIVSLLNSVYTKFDVLMEN--NPDVYKVE
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57.2%;
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%; Pred. No. 6.7e-133;
112; Mismatches 126;
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Q17010; Q17007; Q17008; Q17009;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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EMBL; U42613; AAC47142.1; -.
EMBL; AF017062; AAC47144.2; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of the soluble guanylyl the mosquito Anopheles gambiae."; Insect Mol. Biol. 8:23-30(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caccone A.,
Powell J.R.;
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Caccone A., Garcia B.A., Mathiopoulos K.D.,
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STRAIN-SUA
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                    TAEPPVANTAAAATPKARHSIPEVVKSVPITSLDPAVPELANLGLCKRILASKTSSSGGP
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                                                                                                                                                                                                                                                                                                                                                94;
                                                                                                                                                                                                                                                                                                                                              Score 1761; DB 5;
Pred. No. 1.4e-124;
4; Mismatches 116;
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Best Local S
Matches 249
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MEDLINE-21391941; PubMed-11406623;
Koglin M., Vehse K., Budaeus L., Scholz H., Be
"Nitric Oxide Activates the beta 2 Subunit of
in the Absence of a Second Subunit.";
J. Biol. Chem. 276:30737-30743(2001).
EMBL; AV004153; AAF86581.1; -
Interpro; IPR001054; G_cyclase.
Interpro; IPR001230; PrenyL_site.
Pfam; PF00211; GUANYLATE_CYCLASES_1; UNKNOW
PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS00294; PRENYLATE_CYCLASES_2; 1.
PROSITE; PS00294; PRENYLATE_CYCLASES_2; 1.
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Q91XJ7;
01-DEC-2001
01-DEC-2001
01-MAR-2002
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble guanylyl GUCY1B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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                                                                                                                                        Local Similarity hes 249; Conserv
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                                                                                  MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
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                                                                                                                                          Conservative
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Chordata;
Rodentia;
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                                                                                                                                      Score 1105; D
Pred. No. 6.6e
17; Mismatches
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                                                                                                                                                                                                                                                                               UNKNOWN_1
                                                                                                                                                           .6e-75;
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e Guanylyl Cyclase
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Best Local Sin
Matches 224;
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Q920Q1;
                                                                                                                                                   SUBMITTED (MAR-2001) to the EMBL/GenBank/DDBJ da EMBL; AB058888; BAB68564.1; -.
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1
PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
SEQUENCE 636 AA; 71642 MW; 951DBDE8970E0890
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
Okamoto H., Asakawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                          "cDNA cloning and expression analysis beta2 subunit.";
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Last annotation updat
                                                       Score 983; DB 11;
Pred. No. 8.9e-66;
4; Mismatches 196;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulsc Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M. Parsons J., Percy C., Rifken L., Roopra A., Saunders D. Smaldon N., Smith A., Sonnhammer E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9XTEO;
01-NOV-1999
01-NOV-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                      Peloderinae;
                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditida;
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                                                                                                                                                                       J., Coulson
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditoidea;
                                                     Shownkeen
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Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Wate Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman "2.2 Mb of contiguous nucleotide sequence from chromosc elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1. PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1. PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001054; G_cyclase.
InterPro; IPR001230; Prenyl_site.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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AL008867; CAB15512:1; -
Z99942; CAB15512:1; JOINED.
Q02846; IAWL.
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                                                                                                                                                                                                                                     MNLDDLTRRGLYLSDIPLHDATRDLYLLGEQFREEYKLTQELEILTDRLQLTLRALEDEK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDVEK------LECEDE------LTGTEISCLRLKGQMIYLPEADSILFLCSPSV :: :: | :: |::|||| | :: ||::||| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSFRCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVI--QQRNEEC- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALH----DHLATIY-PGMRA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCSENAKKC:
                                                                                              NVSEYTYRCLMSPENSDPQFHLEHRGPVSMKGKKEPMQVWFLSR
                                                                                                                                                                                                                                                                                                                                                                                                                             TSIPELLQYGLRLTAMPIHDPTRDLILLNQQRLSDVEMNLQLEANNEQLENMAKDLEVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGERIEEHVIFLVKTLNTDQSNEEALGTAVVQHSNN--YKIRLTHMDFISTFPYHMVVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCKIVQVGRELYNHIPKDLLSVGTPLMRIFEVTRPQIPLDFDSICNFINAVEVLQVKTTP
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                                                  ----AESTGRFEFEPRGRVQIKGKGE
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Pred. No. 4.9e-64;
11; Mismatches 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234;
                                                  MNTYFLLR
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dman P.;
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Matches 230
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PRELIMINARY;

P92006;

P92006;

O1-MAY-1997 (TrEMBLrel. 03, Created)

O1-MAY-1997 (TrEMBLrel. 03, Last sequence upd

O1-JUN-2002 (TrEMBLrel. 21, Last annotation u

M04G12.3 protein.

M04G12.3.

Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rh

Rhabditidae; Peloderinae; Caenorhabditis.

NCBL_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS00294; PRENYLATION; UNKNOWN_1.

SEQUENCE 686 AA; 78588 MW; 65AE352DB53CBA57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001054; G_cyclase.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Investigating biology ";
Science 282:2012-2018(1998).
EMBL; Z81103; CAB03210.1; -.
HSSP; P16068; IAWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Sims M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                 DRIQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGENAF::|: | | | : | : | : | : |
                                                                                                                                                                                  SHINTVFVLRSKEGLL------
                                                                                                                                                                                                                                                                                                                                                                          DFSRALPYHFVLDESCRLVQCGDELYNHIPNELLQPGT-PILRIFEINRPQIPLDFENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APSFRCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEEC--
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                                                                                                                                                                                                                                                                                NFINAVFVLQVKTSPLRKKHMNAMTKEEREQEVEAMEEEVESNELTQGCHLKLKGQMMML
                                                                                                                                                                                                                                                                                                                                                                                                                        TFCKAFPFHIIFDRDLVVTQCGNAIYRVLPQ--LQPGNCSLLSVFSLVRPHIDISFHGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPSFRCEENPDGT-LMLHYFTGRPGLYHIVKGVVKEVAKLVFNLDISL-VVQGRTQRSVH
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Query Match Best Local S Matches 220

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076340;
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MEDLINE-99107914; PubMed-9891024;

MIGHORN A., Byrnes K.A., Morton D.B.;

"Identification and characterization of a novel
soluble guanylyl cyclase that is active in the a
subunit and Is relatively insensitive to nitric
J. B101. Chem. 274:2525-2531(1999).

EMBL; AF064514; AAD09836.1;

HSSP; Q02846; IAWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble guanylyl cyclase beta-3.
Manduca sexta (Tobacco hawkmoth (Tobacco hornworm).
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insect
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Sphinglodea; Sphingldae; Sphinglnae; Manduca.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence up
01-UN-2002 (TrEMBLrel. 21, Last annotation
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PS00125; GGANYLATE_CYCLASES_2;
PS00124; PRENYLATION; UNKNOWN_1.
PS001294; PRENYLATION; UNKNOWN_1.
940 AA; 106393 MW; 08956886
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IPRO01054; G_cyclase.
IPR001230; Prenyl_site.
0211; guanylate_cyc; 1.
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01-JUN-2002 (Trem
T04D3.4 protein.
T04D3.4.
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Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
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PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
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InterPro; IPR001230; PrenyL_site.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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HSSP; P19687; LAWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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APSFRCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECD-
                                                                                                                                                                      MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
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                                                        LNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALH---DHLATIY-PGMR
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Ewang R., Dayan P., Dewis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Horst D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylers E., Factor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yell, Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
DR HSSP; 002846; 1AML.
DR FIVBASE. FRANOGROSS. CG4154
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PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
SEQUENCE 690 AA; 78736 MW; 4B736D7413E168AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0038295; CG4154.
InterPro; IPR001525; C5_DNA_meth.
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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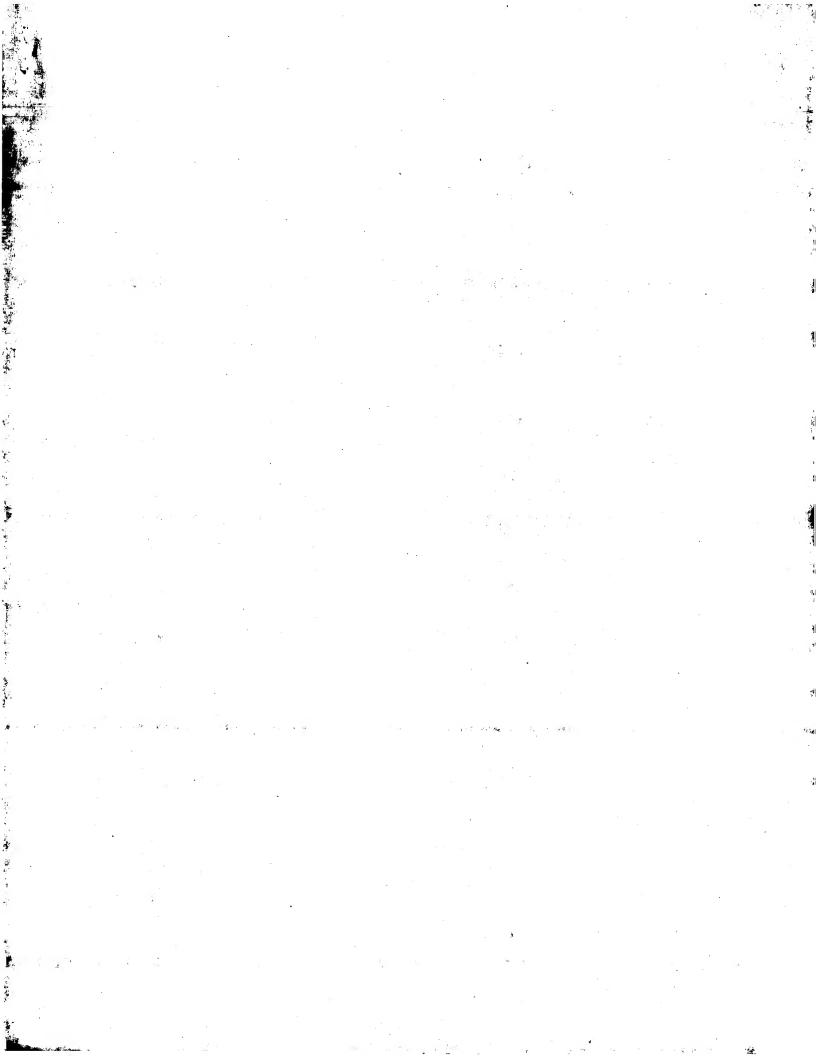
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen
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US-09-473-717-2
US-09-473-717-2
US-09-473-717-3
US-09-726-214-10
US-08-726-214-14
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US-09-74-076-2
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Result

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ANELRHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTD

462 807 354 LLGEQFREEYKLTQELEILTDRLQLTLRALED------EKKKTDTLLYSYLPPSV

Conservative

40;

Mismatches

98;

Indels

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Gaps

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LFHDQKNESY-----MDTLIRRLQLYSRNLEHLVEERTQLYKAERDRADHLNFMLLPRLV

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US-08-894-173-62	08-857	8-80)9-2	-09-324	0-60	9-9	9-9)9-2)9-3	9-0	9-80	9-9)9-2)9-3	9-0	9-8	00 000
94-	57-(57-(JS-09-205-42	24 -	-095-855	-08-997-362	97-(9-205-426-174	24-5	-095-855	-08-997-362-174	97-(2-50	24-5	1-09-095-855	-08-997-362-178	,
173-	-076-	6	CD.	4-542-	355-	362-	-080	126-	42-	355-	62-	7-080-174	126-	42-	355-	362-	ò
62	76	-75	-125	125	125	-125	125	174	174	174	174	US-08-997-080-174	178	178	178	178	
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ALIGNMENTS

; MOLECULE TYPE: protein US-07-623-033-2 RESULT 1 US-07-623-033-2 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 1075 amino acids TYPE: AMINO ACID TOPOLOGY: linear Sequence 2, Application US/07623033 Patent No. 5237051 GENERAL INFORMATION: Query Match Best Local Similarity CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Kohn, Kenneth I. REGISTRATION UNMBER: 30,955 REFERENCE/DOCKET NUMBER: VU9(TELECOMMUNICATION INFORMATION: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Garbers, David L. APPLICANT: Schulz, Stephanie TITLE OF INVENTION: CLONING THE CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: COUNTRY: APPLICATION NUMBER: US/07/623,033 FILING DATE: 19901206 CITY: Chicago ADDRESSEE: 60606-4002 Illinois E: TILTON, FALLON, LUNGMUS & CHESTNUT 100 South Wacker Drive - Suite 960 1075 amino acids 456-8000 12.5%; VU9018 Score 404; DB 1; Pred. No. 4.8e-31; ENTEROTOXIN RECEPTOR Length 1075;

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RESULT 3
US-08-726-214-2
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US-08-864-785-2
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APPLICANT: Raplan, Joshua M.
APPLICANT: Oppenheimer, Allison J.
APPLICANT: Hart, Anne C.
APPLICANT: Hart, Anne C.
TITLE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
TILE REFERENCE: 00786/353001
CURRENT FILING DATE: 1997-05-29
NUMBER OF SEQ ID MOS: 3
SOFTWARE: FESTSEQ for Windows Version 3.0
                                                                              Sequence 2, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 93; Conserv
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LENGTH: 1253
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NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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                                                                                                   ADENYLYL CYCLASE
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US-08-726-214-18
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US-08-726-214-2
                                                                                                                                 Sequence 18, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, We1-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
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Best Local 9
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: Concurren
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                   CORRESPONDENCE ADDRESS:
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                                           STREET: F. STREET: Houston
     COUNTRY: United States ZIP: 77210
                                         STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Highlander, St
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UN
ZIP: 77210
                                                                                                ADDRESSEE:
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                                                                              P.O. Box
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                                                                                Arnold, White & Durkee O. Box 4433
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Pred. No. 1.5e-21;
9; Mismatches 80;
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                           America
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RESULT .5
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                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08726214 Patent No. 6107076
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
              CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acid
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
Annold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                          APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE:
TITLE OF INVENTION: AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/726,214
                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
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                                                                                                                                         77210
                                                                                                                                                                                        Houston
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TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLGLRKWQYDVWSNDVTLANVMEAAGLPGKVHITKTTLACLNGDYEVEP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIGORMPRYCLEGATVALTSRTETTGEKGKINVSEYTYRCLMSPENSDP 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDCYYCVSGLTQPKTDHAHCCVEMGLDMIDTITSVAEATEVD---LNMRVGLHTGRVLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDKYMTVSGLPEPCIHHARSICHLALDMME----IAGQVQVDGESVQITIGIHTGEVVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHDNVSILFADIVGFTGLASQCT----AQELVKLLNELFGKFDELATEN----HCRRIKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYDNVTILESGIVGENAECSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPEVYKVETV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QARNCIEDRLR-----LEDENEKQERLLMSLLPRNVAMEMKEDFLKPPERIFHK--IYIQ
                                                                                                                                                                        Texas
                                                                                                                                                                                                        P.O. Box 4433
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Concurrently Herewith
                                                                                                                                                                                                                                                                       SOLUBLE MAMMALIAN AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 309; DB 3; Length 533; 33.6%; Pred. No. 4.6e-22;
                 US/08/726,214
                                                                                                                                                      of America
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                                                  Version
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                                                                                                                                                                                                                                                                                            ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                      RESULT 6
US-09-473-717-2
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                                                                              GENERAL INFORMATION:
APPLICANT: Storm, Daniel R.
APPLICANT: Hacker, Beth
APPLICANT: Tomlinson, James
                                                                                                                                                  Sequence 2, Application US/09473717 Patent No. 6372475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local S
            APPLICANT: Tomlinson, James E. .
APPLICANT: COR Therapeutics, Inc. .
APPLICANT: University of Washington
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1248 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Highlander, St
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
1115 ASRMDSTGVSGRIQVPEETYLIL-----KDQGFAFDYRGEIYVKGISEQEGKIKTYFL 1167
                                                                                           1055 GHLCALADFSLALTESIQEINKHSFNNFELRIGISHGSVVAGVIGAKKPQYDIWGKTVNL 1114
                                                                                                                                   494 RSICHLALDMMEIAGQVQVDGE----SVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 TSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLEHRGPVSMKGKKE---PMQVWFL 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 MRDEVFKSNLVCAFIVLLFITAIQSLLPSSRLMPMTI--QFSILIMLHSALVLITTAED-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 LAQALHVQSGPE-----EINKRIEHTIDLRSGDKLRREHIKPFSLMFKDSSLEHKYSQ
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                                                                                                                                                                                                                                                                                     NEMKDLREHNENMLRNILPGHVARHFLEKDRDNEELYSQSYDAVGVMFASIPGFADFYSQ
                                                                                                                                                                                          TEMNNQGVECLRLLNEIIADFDELLGEDRFQDIEKIKTIGSTYMAVSGLSPEKQQCEDKW 1054
                                                                                                                                                                                                                          HASGEGAMKIVNLLNDLYTREDTLITDSRKNPEVYKVETVGDKYMTVSGL-PE--PCIHHA 493
                                                                                                                                                                                                                                                                                                                                                                                    GLFLSYDNLNHSGEDFLGTKEASLLLMAMFLLAVFYHGQQLE-YTARLDFLWRVQAKEEI 934
                                                                                                                                                                                                                                                                                                                                                                                                                              GLYLSDIPLHDATRD------LVLLGEQFREEYKLTQELEILTDRLQLTLRA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEDELTGTEI------SCLRLKGQMIYLPEADSILFLCSPSVM-----NLDDLTRR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKCLPLILKTCCWINETYLARNVIIFASILINFLGAV--INILWCDFDKS--IPLKNLT
                                                                                                                                                                                                                                                                                                                                    --LEDEKKKTDTLLYSVLPPSVANEL----RHKRPVPAKRYDNVTILFSGIVGFNAFCSK 436
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Pred. No. 2.2e-21;
""" amatches 209;
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44481-5029-01-US

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PRIOR APPLICATION NUMBER: 0
PRIOR FILING DATE: 1997-07-
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 1294
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus 
US-08-864-785-3
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APPLICANT: Kaplan, Joshua M.
APPLICANT: Oppenheimer, Allison J.
APPLICANT: Hart, Anne C.
APPLICANT: Hart, Anne C.
TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,
TITLE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1305
TYPE: PRT
                                                                                                                                                                                                                               Query Match 9.0%;
Best Local Similarity 31.2%;
Matches 74; Conservative 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 00786/353001
CURRENT APPLICATION NUMBER: US/08/864,785A
CURRENT FILING DATE: 1997-05-29
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/098,559
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/473,717
CURRENT FILING DATE: 1999-12-29
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similarity 31.2%;
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                                                                                                RPVPAKRYDNYTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFV 469
                                                                                                                                                     LEVEKALKERMIHSVMPRIIADDLMKQGDEESENSVKRHATSSPKNRKKKSSIQKAPIAF 382
                                                                                                                                                                                           LEDEKKKTDTLLYSVLPPSVANEL------RHK--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCGILGMRRFKFDVWSNDVNLANLMEQLGVAGKVHISEATAKYL-----DDRYEME 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTGTV 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQ-VQVDGESVQITIGIHTGEV 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPFKMQQIEEVSILFADIVGF----TKMSANKSAHALVGLLNDLFGRFDRLCEETK---C 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPVPAKRYDNYTILFSGIVGENAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFV 469
EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTGTV
                                                                        RPFKMQQIEEVSILFADIVGF----TKMSANKSAHALVGLLNDLFGRFDRLCEQTK---C
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Pred. No. 1.2e-19;
Pred. No. 1.2e-19;
                                                                                                                                                                                                                               Score 291.5; DB 4;
Pred. No. 1.2e-19;
4; Mismatches 72;
                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                      Length 1305;
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495
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                                                                                                                ; OTHER INFORMATION: HYPOTHETICAL: US-09-398-193-2
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; OTHER INFORMATION: HYPOTHETICAL :
US-08-894-173-2
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US-08-894-173-2
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                                                                                                                                                           SEQ ID NO 2
LENGTH: 1353
TYPE: PRT
ORGANISM: Mouse
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LENGTH: 1353
TYPE: PRT
                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09398193 Patent No. 6197581 GENERAL INFORMATION:
APPLICANT: Medical Research Council TITLE OF INVENTION: Adenylate cycla: FILE REFERENCE: P24360-
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local
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CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/894,173A CURRENT FILING DATE: 1997-08-13 NUMBER OF SEQ ID NOS: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Medical Research Council TITLE OF INVENTION: Adenylate cyclase FILE REFERENCE: P14716C
                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                FEATURE:
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383 LEDEKKKTDTLLYSVLPPSVANEL---
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                                               Conservative
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                                                             9.0%;
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                                                             Score 291.5;
Pred. No. 1.
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Pred. No. 1.3e-19;
4; Mismatches 72;
                                                 Mismatches
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RESULT 11
US-08-726-214-10
19-08-726-214-10
; Sequence 10, Application US/08726214
; Patent No. 6107076
; Patent No. 6107076
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US-09-473-717-3
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LENGTH: 1353
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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CURRENT ELING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR FILING DATE: 1998-07-01
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 1997-0
NUMBER OF SEQ ID NOS: 3
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PRIOR FILING DATE: 1997-07-01
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APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
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Similarity 31.2%; Pred. No. 1.
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les 72;
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Best Local Similarity
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TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: AND USES THEREF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Annold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino aci
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                             VGENAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPE 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLVMLAFHAARPPLQVVY------LAVLAAAVGVILIMAVLCNRAAFHQDHM---GL
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                                                                                                                                                                                                                                                                                                                                                                                  LRALEDEKKKTDTLLYSVLPPSVANELR-------HKRPVPAKRYDNVTILFSGI 427
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                                           RKEEKAMIAKMNRORTNS
                                                                           GKKEPMQVWFLSRKNTGT
                                                                                                                  VTLANHMEAGGKAGRIHITKATLNYLNGDYEVEPGCGGERNAYLKEHSIETFLILRCTQK 485
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                                                                                                                                                          VNLTSRTETTGEKGKINVSEYTYRCLMSPENSDP---
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milarity 23.58;
Conservative 84
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474-7577
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Pred. No. 2e-19;
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US-08-726-214-6
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Best Local Similarity 21.88;
Matches 119; Conservative 104
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GENERAL INFORMATION:
APPLICANT: Tang, F
APPLICANT: Gilman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08726214 Patent No. 6107076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1144 amino aci
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 6
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
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ZIP: 77210
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MKIVNLLNDLYTREDTLTDSRKNPEVYKVETVGDKYMTVSGLPEPCIH-
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                                 {\tt RWNEALVTNMLPEHVARHFLGSKKRDEELYSQSYDEIGVMFASLPNFADFYTEESINNGG}
                                                                     --TDTLLYSVLPPSVANEL----RHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGA
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Pred. No. 3.1e-19;
14; Mismatches 201;
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US-09-398-193-99
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Patent No. 6107076
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TYPE: PRT
                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
COMPUTER READABLE
                                                      STATE:
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                   COUNTRY: United States ZIP: 77210
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                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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                                                      Houston: Texas
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30.8%; Pred. No. 8.2e-19;
                                                                                                                                                                                   SOLUBLE MAMMALIAN ADENYLYL CYCLASE
                                      of America
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                                                   PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-07
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-07
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09474076 Patent No. 6465237
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                                                                                                                                                                                      FILE REFERENCE: 44481-5028-01-US CURRENT APPLICATION NUMBER: US/09/474,076 CURRENT FILING DATE: 1999-12-12
                                                                                                                                                                                                                                               TITLE OF INVENTION: CLONING
TITLE OF INVENTION: CYCLASE
                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                      SOFTWARE:
LENGTH: 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Highlander Steven L.
REGISTION NUMBER: 37.642
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 29.3 hes 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/005,498 FILING DATE: 04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 TRRGLYLSDIPLHDATRDLVLLGEQFREEY-----KLTQELEILTDRLQLTLRALEDEK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 SLANRMEAAGVPGRVHITEATLNHL-----DKAYEVEDGHGEQRDP 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 LPTHARNCVKMGLDICEAIKQVREATGVDISMRVGIHSGNVLCGVIGLRKWQYDVWSHDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 KKTDTLLYSVLPPSVANEL------RHKRP-----VPAKRYDNVTILFSGIV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIHHARSICHLALDMMEIAGQV-QVDGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                    PatentIn Ver.
                                                                                                                                                                                                                                                                    Tomlinson, James E.

COR Therapeutics, Inc.

VENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQF-----HLEHRGP 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GF----TRLASDCSPKELVVVLNELFGKFDQIAKANE---CMRIKILGDCYYCVSGLPVS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFNAFCSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPFVYKVETVGDKYMTVSGLPEP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROQENLLLSVLPAHISMGMKLAIIERLKEGGDRHYMPDNNFHSLYVKRHQNVSILYADIV
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1998-07-01
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Pred. No. 7.2e-19;
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Best Local Similarity
   526
                                     574 SPENSDP-----QFHLEH---RGPVSMKGKKEPMQVWFLSRKNTGTEE 613
                                                                            466
                                                                                                              514 GESVQITIGIHTGEVVTGVIGQRMPRYCLEGNTVNLTSRTETTGEKGKINVSEYTYRCLM 573
                                                                                                                                                   409 ARFDKLAAEN---HCLRIKILGDCYYCVSGLPEARADHAHCCVEMGVDMIEAISLVREVT 465
                                                                                                                                                                                      455 TREDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQV-QVD 513
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                                                                                                                                                                                                                                                                                                                                                                                 262 LSGLGLSTLHLILAWQLNRGDAFLWKQLGANVLLFLCT----
                                                                                                                                                                                                                                                                                                                                                                                                       296 LTGTEISCLRL------KGQMIYLPE--ADSILFLCSPSVMNLDDLTRRGLYLSDIPLH 346
                                                                                                                                                                                                                                                                                                                        DATROLVILIGEQFREEYKLTQELEILTDRIQLTLRALEDEKKKTDTILIYSVLPPSVANEL 406
                                                                        GVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHMEAGGRAGRIHITRATLQYLN
                                                                                                                                                                                                                            KEDINTKKEDMMFHK--IYIQKHDNVSILFADIEGFTSLASQCT----AQELVMTLNELF 408
                                                                                                                                                                                                                                                               R------HKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLY
                                                                                                                                                                                                                                                                                                       ----NVIGICTHYPAEVSQRQAFQETRGYIQARLH-LQHENRQQERLLLSVLPQHVAMEM
GDYEVEPGRGGERNAYLKEQHIETFLILG-ASQKRKEEKAMLAKLQRTRANSME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 282.5; DB 4;
Pred. No. 8e-19;
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Search completed: June 27, 2003, 13:05:59
Job time: 14.7678 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 13:05:32; Search time 32.6287 Seconds (without alignments) 2080.112 Million cell updates/sec

Title: Perfect score: US-09-762-767A-4 3231 1 MYGFVNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

424699 segs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database Published_Applications_AA: *

4: 6: 7: 7: 10: 110: 113: 113: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/TSO6_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/TSO6_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	BIG	ID	Description
1	789.5	24.4	069	į į	US-10-205-823-162	Sequence 162, App
N	778	24.1	691	9	US-09-952-213D-2	
ω	407.5	12.6	1073	10	US-09-819-249-2	D 22
4	405.5	12.6	1073	9	US-10-157-031-18	•
ഗ	291.5	9.0	1294	12	US-10-071-223-2	2
0	291.5	9.0	1353	10	US-09-751-100B-2	N
7	291.5	9.0	1353	12	US-10-071-223-3	ω
8	289	8.9	1080	ø	US-10-282-942-2	
9	283.5	8.8	1353	10	US-09-751-100B-99	Sequence 99, Appl
10	282.5	8.7	1168	9	US-10-201-000-2	Sequence 2, Appli
11	282.5	8.7	1168	10	US-09-750-240-11	Sequence 11, Appl
12	278.5	8.6	604	10	US-09-750-240-4	
13	278.5	8.6	1167	10	US-09-750-240-6	6
14	278	8.6	1261	9	US-10-175-158-2	,
15	269.5	8.3	257	9	US-09-989-442-95	
16	269.5	8.3	302	10	US-09-915-582-50	U
17	269.5	8.3	1077	9	us-10-121-911-1	
18	265.5	8.2	1167	10	US-09-750-240-13	Sequence 13, Appl
19	264	8.2	241	9	US-09-764-868-794	Sequence 794, App

Query Match Best Local Similarity

24.4%; 35.1%;

Score 789.5; DB 9; Pred. No. 5.3e-60;

Length 690;

ALIGNMENTS

US-10-205-823-162		; LENGTH: 690	SEQ ID NO 162	SOFTWARE: Fastseo for Windows Version 4.0	· NIMBER OF SEC ID NOS. ASS		; PRIOR APPLICATION NUMBER: 60/341,746	; PRIOR FILING DATE: 2001-09-25	FILING DATE	; PRIOR FILING DATE: 2001-07-25	; PRIOR APPLICATION NUMBER: 60/307,982	; CURRENT FILING DATE: 2002-07-25	; CURRENT APPLICATION NUMBER: US/10/205,823	Ċ	INVENTION: THERAPY OF PROSTATE CANCER	INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,	; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND	; APPLICANT: Anderson, Dustin	••	 ••	••	••	; APPLICANT: Gorbatcheva, Bella	; APPLICANT: Gannavarapu, Manjula	 ; APPLICANT: Monahan, John E.	; APPLICANT: Schlegel, Robert	; GENERAL INFORMATION:	; Publication No. US20030108963A1	; Sequence 162, Application US/10205823	US-10-205-823-162	TIPSE	
•	,															PREVENTION, AND																

Matches

207;

101

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RESULT 2
US-09-952-213D-2
; Sequence 2, Application US/09952213D
; Publication No. US20030096240A1
                                                                                                                                                                                                                                                                                                                             APPLICANT: KRUMENACKER, J. S.
APPLICANT: MARTIN, E.
TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND
FILE REFERENCE: UTSH: 252US
CURRENT APPLICATION NUMBER: US/09/952,213D
CURRENT FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 15
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                                                                                                                          il Similarity 33.5
213; Conservative
                                                               LELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEILQ 68
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                                           LNLALQRTLAKHKIEENRKSSEKED----LEKIIAEEA----IAAGAPVEALK-----D
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  MFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHARSICHLALDMMEIAGQV-QVDGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPG
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                                                                                                                          Score 778; DB 9;
Pred. No. 5.3e-59;
DS; Mismatches 224;
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                                                                                                                                                                    Length 691;
  HDHLATIYPGMRAPSFRCT 123
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                                                                                                                          Gaps
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-249-2
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CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/192,229
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09819249 Patent No. US20010029019A1
                                                                                                                                                                                       Query Match
                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Waldman, Scott A.
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods
TITLE OF INVENTION: Alimentary Canal Origin
FILE REFERENCE: TJUZ412
                                                           245 VIIMCGGPEFLYKLKGDRAVAEDIVIILVDLFNDQYLEDNVTAPDYMKNVLVLTLSPGNS 304
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                                                                                                                                              Conservative
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Pred. No. 2e-26;
7; Mismatches 2
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; ORGANISM: Mus musculus US-09-952-213D-2

Query Match Best Local

NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 2
LENGTH: 691
TYPE: PRT

APPLICANT: MURAD, APPLICANT: SHARIN

SHARINA,

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US-10-157-031-18
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                     ; ORGANISM: Homo sapiens US-10-157-031-18
                                                     NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 1073
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/10157031 Publication No. US20030108890A1
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                              APPLICANT: Baranova, A. V.
APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed
                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/157,031 CURRENT FILING DATE: 2002-05-30
                                                                                                                                                                                      FILE REFERENCE: 2760-103
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US-10-071-223-2
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PRIOR FILING DATE: 1999-12-29
PRIOR PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/098,559
PRIOR APPLICATION NUMBER: 08/886,440
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 2
LENGTH: 1294
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APPLICANT: Storm, Daniel
APPLICANT: Hacker, Beth
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 12
TYPE: PRT
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                                                                                                                                                                                                                                                                           Local
                                    436
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APPLICANT: COR Therapeutics, Inc.
APPLICANT: University of Washington
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5029-02-US
CURRENT APPLICATION NUMBER: US/10/071,223
CURRENT FILING DATE: 2002-02-11
                                                                                                                                                                                                                                                                323 LEVEKALKERMIHSVMPRIIADDLMKQGDEESENSVKRHATSSPKNRKKKSSIQKAPIAF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 LLGEQFREEYKLTQELEILTDRLQLTLRALED-----
                                                                                                                                                                                                                                                                                                                        383 LEDEKKKTDTLLYSVLPPSVANEL------RHK---
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                                                                                        YKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQ-VQVDGESVQITIGIHTGEV 528
                                                                                                                                                                                                               RPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFV 469
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VTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLE
                                                       EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTGTV
                                                                                                                                                                                                                                                                                                                                                                       Score 291.5; DB 12.
Pred. No. 3.5e-16;
4; Mismatches 72;
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RESULT 7
US-10-071-223-3
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US-09-751-100B-2
US-10-071-223-3
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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                                                                                                                                                                      SEQ ID NO 3
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TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/098,559
PRIOR FILING DATE: 1997-07-01
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CURRENT APPLICATION NUMBER: US/10/071,223
CURRENT FILING DATE: 2002-02-11
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                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/886,440
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: COR Therapeutics, Inc.
APPLICANT: University of Washington
TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
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                               ORGANISM: murine
                                                                                                                         LENGTH:
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| :::| | | : : | | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | | :::| | | :::| | | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | | ::::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | 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                                   type IX adenylyl cyclase
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Pred. No. 3.7e-16;
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Sequence 2, Application US/10282942
Publication No. US20030087295A1
GENERAL INFORMATION:
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS FOR
FILE REFERENCE: MPI01-240PIRM
CURRENT APPLICATION NUMBER: US/10/282,942
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 60/335,047
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 2
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-282-942-2
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US-10-282-942-2
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Best Local S
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                                                                                                                                                                                                                                                                                                                    356 GEQFREEYKLTQELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVA------------ 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 VYTLLPFSMRGAVAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 IYRVLPQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDE 295
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                                                                                                                                                                                                                                                                                                                                                              168 --GFTTPSVRVGLQLL----ANAVIFLCG----NLTGAFHKH-----QMQDASRDL---
                                                                                                                                                                                                                                                                                                                                                                                                        296 LTGTEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLL 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 8.9%;
Similarity 26.3%;
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DINMRVGIHSGNVLCGVIGLRKWQYDVWSHDVSLANRMEAAGVPGRVHITEATLKHL
                                          SVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCL 572
                                                                                        FDQIAKANE---CMRIKILGDCYYCVSGLPVSLPTHARNCVKMGLDMCQAIKQVREATGV 367
                                                                                                                                                                                                                    ELRHKRPVP-----AKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTR 456
                                                                                                                                  FDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQV-QVDGE 515
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                                                                                                                                                                                                                                                                        -----FTYTVKCIQIR-----RKLRIEKRQQENLLLSVLPAHISMGMKLAIIERLK 254
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31.2%; pred. No. 3.7e-16;
34. Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Mismatches 109;
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Pred. No. 4.4e-16;
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                                                                                                                                               ; LENGTH: 1168
; TYPE: PRT
; ORGANIZSM: human type VI adenylyl cyclase
US-10-201-000-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10201000 Publication No. US20020187540A1 GENERAL INFORMATION:
                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
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LENGTH: 1353
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                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/474,076
PRIOR FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: PCT/US98/13694
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,904
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-US
CURRENT APPLICATION NUMBER: US/10/201,000
CURRENT FILING DATE: 2002-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/751,100B
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tomlinson, James E.
APPLICANT: COR Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P27948A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human Adenylate Cyclase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Medical Research Council
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                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/886,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 VTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLE 585
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262 LSGLGLSTLHLILAWQLNRGDAFLWKQLGANVLLFLCT
                                296 LTGTEISCLRL------KGQMIYLPE--ADSILFLCSPSVMNLDDLTRRGLYLSDIPLH 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTRTV 495
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                                                                                            Similarity
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                                                                        Conservative
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                                                                                          8.7%;
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Pred. No. 1.9e-15;
4; Mismatches 73;
                                                                                      Score 282.5; DB 9; Pred. No. 1.8e-15;
                                                                        Mismatches
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                                                                                                         Length 1168;
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US-09-750-240-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-5
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
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SEQ ID NO 11
LENGTH: 1168
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Best Local
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE TITLE OF INVENTION: FAILURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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455 TREDTLTDSRKNPEVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQV-QVD
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                                                                                                                                                                                                                                                                                                                               94;
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                                             KEDINTKKEDMMFHK--IYIQKHDNVSILFADIEGFTSLASQCT----AQELVMTLNELF
                                                                                                                                      ----NVIGICTHYPAEVSQRQAFQETRGYIQARLH-LQHENRQQERLLLSVLPQHVAMEM
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26.6%;
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                                                                                        -HKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLY 454
                                                                                                                                                                                                                                                                                                                           ; Score 282.5; DE; Pred. No. 1.8e-1 61; Mismatches 1
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US-09-750-240-4
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PRIOR FILING DATE: 1999-12-27
PRIOR PEPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-76
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.6%;
Best Local Similarity 27.1%;
Matches 83; Conservative 5
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TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/708,661 PRIOR FILING DATE: 1996-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/750,240 CURRENT FILING DATE: 2001-10-12
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                                                                                                                              515
                          315 DYEVEP 320
                                                           575 PENSDP 580
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                                                                                                                           ESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMS
                                                                                                                                                            RFDKLAAEN---HCLRIKILGDCYYCVSGLPEARADHAHCCVEMGVDMIEAISLVREVTG
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US-10-175-158-2
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US-09-750-240-6
Sequence 2, Application US/10175158

Publication No. US2003000371A1

GENERAL INFORMATION:
APPLICANT: Tomlinson, James
APPLICANT: Cor Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 4481-5027-01-US
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Best Local Similarity
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Post, S. R.
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TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-01-16
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 08/048,933
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR FILING DATE: 1996-09-05
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466 VNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHMEAGSRAGRIHITRATLQYLNG
                                                                                                                                                                                                                                                                                                                                                            300 ----NVISICTHYPAEVSQRQAFQETRSYIQARLH-LQHENRQQERLLLSVLPQHVAMEM
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                                                  ESVQITIGIHTGEVVTGVIGQRMPRYCLEGNTVNLTSRTETTGEKGKINVSEYTYRCLMS
                                                                                                                       RFDKLAAEN---HCLRIKILGDCYYCVSGLPEARADHAHCCVEMGVDMIEAISLVREVTG
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Pred. No. 4e-15;
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NUMBER: US/10/175,158

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HUMAN ADENYLYL

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; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: human type V adenylyl cyclase
US-10-175-158-2
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PRIOR APPLICATION NUMBER: US/09/473,716
PRIOR FILING DATE: 1999-12-29
PRIOR PPLICATION NUMBER: PCT/US98/13540
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,901
PRIOR APPLICATION NUMBER: 60/070,901
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 2
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Publication No. US20030013649A1
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Best Local :
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PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/989,442
CURRENT FILING DATE: 2001-11-21
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                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Rosen et al
                                                                                                                                                                                                                                                                                                                                                                                     ILE REFERENCE: PJZ08
                                                                                                                                                                                                                                                                                                                                                                                                 TLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                            APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
                                                                                                                                                                                                            APPLICATION NUMBER: 60/214,886 FILING DATE: 2000-06-28 APPLICATION NUMBER: 60/217,487 FILING DATE: 2000-07-11
                                                                                                                                                              APPLICATION NUMBER: 60/220,963
                                                                                                                                                                                               APPLICATION NUMBER: 60/225,758
                          APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14 APPLICATION NUMBER: 60/225,757
                                                                                                                                              FILING DATE: 2000-07-26
APPLICATION
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Pred. No. 5e-15;
7; Mismatches
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FILING DATE: 2000-08-1
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FILING DATE: 2000-07-26
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FILING DATE: 2000-09-25
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APPLICATION NUMBER: 60/249,215
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APPLICATION NUMBER: 60/231,414 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/231,244
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Search completed: June 27, Job time : 34.6287 secs 2003, 13:17:13